

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 17:00:32 ; Search time 38 Seconds
(without alignments)
192.383 Million cell updates/sec

Title: 07330446.PSP

Perfect score: 405

Sequence: 1 qpdaipvtccynftrki.....qkvwgdmhldkqtgptk 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 405 | 100.0 | 99 | 2 A60299 | monocyte chemoattr |
| 2 | 337 | 83.2 | 99 | 2 JC2136 | monocyte chemoattr |
| 3 | 315 | 77.8 | 99 | 1 A39296 | monocyte chemoattr |
| 4 | 315 | 77.8 | 99 | 2 JC2336 | monocyte chemoattr |
| 5 | 314 | 77.5 | 125 | 2 I46857 | monocyte chemoattr |
| 6 | 288 | 71.1 | 72 | 2 A55984 | monocyte chemoattr |
| 7 | 287 | 70.9 | 109 | 2 A54678 | monocyte chemoattr |
| 8 | 270 | 66.7 | 97 | 2 JC4912 | ectaxin precursor |
| 9 | 268 | 66.2 | 99 | 2 JC5295 | monocyte chemoattr |
| 10 | 261 | 64.4 | 99 | 2 JC2417 | monocyte chemoattr |
| 11 | 252 | 62.2 | 148 | 1 A30209 | PDGF-inducible JE |
| 12 | 241 | 59.5 | 148 | 1 S07723 | immediate-early se |
| 13 | 236 | 58.3 | 120 | 2 I48147 | monocyte chemoattr |
| 14 | 214 | 52.8 | 96 | 2 I48099 | ectaxin precursor |
| 15 | 207 | 51.1 | 96 | 2 JC2478 | ectaxin precursor |
| 16 | 200 | 49.4 | 97 | 2 A48093 | monocytic cytokine |
| 17 | 145.5 | 35.9 | 93 | 2 B35673 | LD78-beta protein |
| 18 | 142.5 | 35.2 | 92 | 2 A30574 | macrophage inflam |
| 19 | 135.5 | 33.5 | 92 | 1 A31767 | macrophage inflam |
| 20 | 133.5 | 33.0 | 92 | 2 I46730 | immune activation |
| 21 | 127.5 | 31.5 | 92 | 2 C30552 | macrophage inflam |
| 22 | 123 | 30.4 | 92 | 2 I52322 | macrophage inflam |
| 23 | 119 | 29.4 | 92 | 2 A32393 | macrophage inflam |
| 24 | 108.5 | 26.8 | 91 | 1 A46539 | monocyte chemoattr |
| 25 | 106 | 26.2 | 120 | 2 JE0177 | lymphocyte and mon |
| 26 | 105.5 | 26.0 | 91 | 1 A28815 | monocyte chemoattr |
| 27 | 99.5 | 24.6 | 96 | 2 A37236 | I-309 protein prec |
| 28 | 99.5 | 24.6 | 114 | 2 E37UL | lymphotactin precu |
| 29 | 98 | 24.2 | 50 | 2 C60407 | monocyte adherence |

30 94 23.2 103 2 A53096 interleukin-8 prec
31 93.5 23.1 92 2 S24236 TCA3 protein - mou
32 91.5 22.6 114 1 BTMSL lymphotactin precu
33 83 20.5 101 2 I48148 Neutrophil attract
34 79 19.5 101 2 S42496 interleukin-8 prec
35 79 19.5 101 2 I46871 interleukin-8 - ra
36 75 18.5 95 2 JN0841 interleukin-8 - do
37 73.5 18.1 116 2 I49555 gene C10 protein -
38 70 17.3 99 2 A37034 interleukin-8 prec
39 66 16.3 2867 2 AG3481 cellobiose-phospho
40 65.5 16.2 143 2 S76162 hypotheical prote
41 65 16.0 282 2 S44825 hypotheical prote
42 64.5 15.9 363 2 T26700 hypotheical prote
43 64 15.8 1019 2 E90097 hypotheical prote
44 64 15.8 1076 2 F96831 hypotheical prote
45 62.5 15.4 853 2 AB2020 hypotheical prote

ALIGNMENTS

RESULT 1

A60299

monocyte chemoattractant protein 1 precursor - human

N/Alternate names: GDCP-1; glioma-derived monocyte chemotactic factor 1; MCAF; MCP-1; mon
N/Contains: glioma-derived chemotactic factor 2 (GDCP-2)

C/Species: Homo sapiens (man)

C/Date: 20-Feb-1993 #sequence, revision 20-Feb-1993 #text change 16-Jul-1999

C/Accession: A35474; A33476; S03339; I51841; A60299; A32300; A32396; A34561; I57488; JCI1

R:Shyy, Y.J.; Li, Y.S.; Kolattukudy, P.E.

Biochem. Biophys. Res. Commun. 169, 346-351, 1990

A/Title: Structure of human monocyte chemotactic protein gene and its regulation by TPA.

A/Reference number: A35474; MUID:90290466; PMID:2357211

A/Accession: A35474

A/Molecule type: DNA

A/Residues: 1-99 <SHY>

A/Cross-references: GB:M37719; NID:G187447; PIDN:AAA18102.1; PID:G487124

R:Rollins, B.J.; Stier, P.; Ernest, T.; Wong, G.G.

Mol. Cell. Biol. 9, 4687-4695, 1989

A/Title: The human homolog of the ~~chemo~~ gene encodes a monocyte secretory protein.

A/Reference number: A33476; MUID:90097880; PMID:2513477

A/Accession: A33476

A/Molecule type: mRNA

A/Residues: 1-99 <ROI>

A/Cross-references: GB:M30816; GB:M31625; GB:M31626; NID:G188701; PIDN:AAA36330.1; PID:G

R:Yoshimura, T.; Fukui, N.; Moore, S.K.; Appella, E.; Lerman, M.I.; Leonard, E.J.

FEBS Lett. 244, 487-493, 1989

A/Title: Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, exp

A/Reference number: S03339; MUID:89153605; PMID:2465924

A/Accession: S03339

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-99 <YOS>

A/Cross-references: GB:X14768; NID:G34513; PIDN:CAA32876.1; PID:G34514

A/Experimental source: glioma cell line U-105MG

R:Yoshimura, T.; Leonard, E.J.

Adv. Exp. Med. Biol. 305, 47-56, 1991

A/Title: Human monocyte chemoattractant protein-1 (MCP-1).

A/Reference number: I51841; MUID:92095166; PMID:1661560

A/Accession: I51841

A/Status: preliminary; translated from GB/EMBL/DDEJ

A/Molecule type: mRNA

A/Residues: 1-99 <YOS>

A/Cross-references: GB:S71513; NID:G240867; PIDN:AA20651.1; PID:G240868

R:Bottazzi, B.; Colotta, F.; Salca, A.; Nobili, N.; Mantovani, A.

Int. J. Cancer 45, 795-797, 1990

A/Title: A chemoattractant expressed in human sarcoma cells (tumor-derived chemotactic f

-1/MCAF).

A/Reference number: A60299; MUID:90216082; PMID:2182547

A/Accession: A60299

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A;Residues: 1-99 <BOT>
R;Furtani, Y.; Nomura, H.; Notake, M.; Oyama, Y.; Fukui, T.; Yamada, M.; Larsen, C.G.
Biochem. Biophys. Res. Commun. 159, 249-255, 1989
A;Title: Cloning and sequencing of the cDNA for human monocyte chemoattractant and activation
A;Reference number: A32300; MUID:89165862; PMID:2923622
A;Accession: A32300
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-99 <FUR>
A;Cross-references: GB:M24545; NID:G187434; PIDN:AAA18164.1; PID:G307163
R;Robinson, E.A.; Yoshimura, T.; Leonard, E.J.; Tanaka, S.; Griffin, P.R.; Shabanowitz,
Proc. Natl. Acad. Sci. U.S.A. 86, 1850-1854, 1989
A;Title: Complete amino acid sequence of a human monocyte chemoattractant, a putative me
A;Reference number: A32396; MUID:89184525; PMID:2648385
A;Accession: A32396
A;Molecule type: protein
A;Residues: 'X', 25-99 <ROB>
R;Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.
Biochem. Biophys. Res. Commun. 157, 904-909, 1990
A;Title: Identification of the monocyte chemoattractant protein from human osteosarcoma cell
A;Reference number: A34561; MUID:90211336; PMID:2322886
A;Accession: A34561
A;Molecule type: protein
A;Residues: 29-33, 'XX', 36-52; 82-92 <DEC>
R;Li, Y.S.; Shyy, Y.J.; Wright, J.G.; Valente, A.J.; Cornhill, J.F.; Kolattukudy, P.E.
Mol. Cell. Biochem. 126, 61-69, 1993
A;Title: The expression of monocyte chemoattractant protein (MCP-1) in human vascular endoth
A;Reference number: I57488; MUID:94150478; PMID:8107690
A;Accession: I57488
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-99 <LY>
A;Cross-references: GB:S69738; NID:G545464; PIDN:AA829926.1; PID:G545465
R;Ye, Q.N.; Su, G.F.; Yuan, Y.; Huang, C.F.
Chinese J. Microbiol. Immunol. 14, 29-32, 1994
A;Title: The PCR, cloning and sequencing of human monocyte chemoattractant protein-1 (MCP
A;Reference number: JCI1096
A;Accession: JCI1096
A;Molecule type: mRNA
A;Residues: 24-28, 'Q', 30-99 <YEQ>
C;Genetics:
A;Gene: GDB:SCY2
A;Cross-references: GDB:125279; OMIM:158105
A;Map position: 17q11.2-17q12
C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine; glycoprotein; inflammation; pyroglutamic acid
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemoattractant protein 1 #status experimental <MAT>
F;24-99/Product: monocyte chemoattractant protein 1, short form #status experimental <MA
F;24/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimen
F;37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5e-39;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPK 76
DB 84 QDSMDHLDKQTQTPK 99

RESULT 2
JC2136
monocyte chemoattractant protein-1 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 16-Jul-1999
A;Accession: JC2136; S57498
R;Hosang, K.; Knoke, I.; Klaudivy, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994

A;Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Analysis
A;Reference number: JC2136; MUID:94183284; PMID:7510962
A;Accession: JC2136
A;Molecule type: mRNA
A;Residues: 1-99 <HOS>
A;Cross-references: GB:Z48479; NID:G683716; PIDN:CAA88370.1; PID:G683717
R;Zach, O.
submitted to the EMBL Data Library, July 1994
A;Reference number: S57497
A;Accession: S57498
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-99 <ZAC>
A;Cross-references: EMBL:X79416; NID:G872312; PIDN:CAAS5945.1; PID:G872313
C;Superfamily: macrophage inflammatory protein
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
F;94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.2%; Score 337; DB 2; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.1e-31;
Matches 60; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPK 75
DB 84 QDSMDHLDKQTQTPK 98

RESULT 3
A32996
monocyte chemoattractant protein 1 precursor - bovine
N;Alternate names: monocyte chemoattractant factor 1; seminal plasma protein P6
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A32996; B3296
R;Wempe, F.; Henschen, A.; Scheit, K.H.
DNA Cell Biol. 10, 671-679, 1991
A;Title: Gene expression and cDNA cloning identified a major basic protein constituent of
A;Reference number: A32996; MUID:92096117; PMID:1721821
A;Accession: A32996
A;Molecule type: mRNA
A;Residues: 1-99 <WEM>
A;Cross-references: GB:M84602; GB:M85264; NID:G163394; PIDN:AAA30651.1; PID:G163395
A;Accession: B32996
A;Molecule type: protein
A;Residues: 50-68, 'X', 70-74, 'X', 76 <WE2>
A;Experimental source: seminal vesicle
C;Superfamily: macrophage inflammatory protein
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemoattractant protein 1 #status predicted <MAT>
F;94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 77.8%; Score 315; DB 1; Length 99;
Best Local Similarity 73.3%; Pred. No. 5.3e-29;
Matches 55; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPK 75
DB 84 QDSMDHLDKQTQTPK 98

RESULT 4
JC2336

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C:Superfamily: macrophage inflammatory protein

Query Match          71.1%; Score 288; DB 2; Length 72;
Best Local Similarity 74.0%; Pred. No. 4.9e-26;
Matches 54; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

QY 3 DAINAPVTCVNFNRKISVORLASYSRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 DAINSPVTCCTLTSTKISMQRLMSYRVTSSKCPKEAVIFKTIAGKEIXAEP--KWWQD 58
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 63 SMDHLDKQTQTPK 75
      ||:||||:||||
DB 59 SISHLDKKNQXPK 71
      ||:||||:||||

RESULT 7
A54678
monocyte chemotactic protein 3 precursor - human
N;Alternate names: monocyte chemoattractant protein MCP-3
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text_change 16-Jul-1999
C;Accession: A54678; JCI1478; S32222
R;Opdenakker, G.; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G.
Genomics 21, 403-408, 1994
A;Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the
A;Reference number: A54678; MUID:94375065; PMID:7916328
A;Accession: A54678
A:Molecule type: DNA
A;Residues: 1-109 <ORD>
A;Cross-references: GB:X72309
R;Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
Biochem. Biophys. Res. Commun. 191, 535-542, 1993
A;Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA and
A;Reference number: JCI1478; MUID:93213290; PMID:8461011
A;Accession: JCI1478
A:Molecule type: mRNA
A;Residues: 1-109 <ORD>
A;Cross-references: GB:X72308; GB:S57464; NID:93928270; PID:CAA51055.1; PID:g313708
R;Minty, A.; Chalon, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Miloux,
submitted to the EMBL Data Library, March 1993
A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoatrac
A;Reference number: S32222
A;Accession: S32222
A:Molecule type: mRNA
A;Residues: 1-109 <MIN>
A;Cross-references: EMBL:X71087; NID:9288396; PID:CAA50405.1; PID:g288397
C;Comment: This protein induces proteinase secretion and chemotaxis by macrophages and m
C;Genetics:
A;Gene: GDB:SCYA7; SCYA6; MCP-3
A;Cross-references: GDB:I38473; OMIM:158106
A;Map position: 17q11-17q12
A;Introns: 36/1; 75/2
C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine; glycoprotein; inflammation
E;1-33/Domain: signal sequence #status predicted <SIG>
F;34-109/Product: monocyte chemotactic protein 3 #status predicted <MAT>
F;39/Binding site: carbohydrate (Asn) #status predicted

Query Match          70.9%; Score 287; DB 2; Length 109;
Best Local Similarity 72.0%; Pred. No. 9.6e-26;
Matches 54; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNRKISVORLASYSRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 34 QPVGINTSTTCYRFINKKIPKQRLSYRVTSSHCPRFAVIFKTIKDKICADPTQKWV 93
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 QDSMDHLDKQTQTPK 75
      |||||:||||:||||
DB 94 QDFMKHLDDKKTQTPK 108
      |||||:||||:||||

RESULT 8
JC4912

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N:Alternate names: monocyte chemoattractant protein-1
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S07723; JN0128
R:Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Nucleic Acids Res. 18, 23-34, 1990
A:Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential
A:Reference number: S07723; MUID:90174947; PMID:2106664
A:Accession: S07723
A:Molecule type: DNA
A:Residues: 1-148 <TIM>
A:Cross-references: EMBL:X17053; NID:g55530; PIDN:CAA34901.1; PID:g55531
R:Yoshimura, T.; Takeya, M.; Takahashi, K.
Biochem. Biophys. Res. Commun. 174, 504-509, 1991
A:Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its exp
A:Reference number: JN0128; MUID:91128376; PMID:1704226
A:Accession: JN0128
A:Molecule type: mRNA
A:Residues: 1-148 <YOS>
A:Cross-references: GB:M57441; NID:g205333; PIDN:AAA63496.1; PID:g205334
A:Experimental source: spleen cells
A:Note: the authors translated the codon GAA for residue 62 as Lys and GGT for residue 6
C:Genetics: 26/1; 65/2
A:Introns:
C:Superfamily: macrophage inflammatory protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>

Query Match 59.5%; Score 241; DB 1; Length 148;
Best Local Similarity 55.3%; Pred. No. 2.4e-20; Indels 0; Gaps 0;
Matches 42; Conservative 16; Mismatches 18

QY 1 QPDAINAPVTCVNFTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
DB 24 QPDVAVNAPLTCVSYFTGKMPKSLNRYKRITSSRCPEAVVFTKLKEICADPNKEWV 83

QY 61 QDSMDHLDKQTQPKT 76
DB 84 QKYIRKLDQNVASET 99

RESULT 13
I48147
monocyte chemoattractant protein-1 - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I48147
R:Yoshimura, T.
J. Immunol. 150, 5025-5032, 1993
A:Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression of
A:Reference number: I48147; MUID:93267104; PMID:8496603
A:Accession: I48147
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-120 <RES>
A:Cross-references: GB:L04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
C:Genetics:
A:Gene: MCP-1
C:Superfamily: macrophage inflammatory protein

Query Match 58.3%; Score 236; DB 2; Length 120;
Best Local Similarity 59.7%; Pred. No. 7.4e-20;
Matches 43; Conservative 14; Mismatches 13; Indels 2; Gaps 2;

QY 1 QPDAINAPVTCVNFTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
DB 24 QPDGVNTP-TCCVTF-NKQPLKRVKGYRITSSRCPEAVIFRTLNKEVCADPTQRWV 81

QY 61 QDSMDHLDKQTO 72
DB 82 QDIYAKUCQRIQ 93

RESULT 14
I48099
eotaxin precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I48099
R:Rothenberg, M.E.; Luster, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.
J. Exp. Med. 181, 1211-1216, 1995
A:Title: Constitutive and allergen-induced expression of eotaxin mRNA in the guinea pig
A:Reference number: I48099; MUID:95173589; PMID:7869037
A:Accession: I48099
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-96 <RES>
A:Cross-references: EMBL:U18941; NID:g687655; PIDN:AAC52180.1; PID:g687656
C:Superfamily: macrophage inflammatory protein

Query Match 52.8%; Score 214; DB 2; Length 96;
Best Local Similarity 57.4%; Pred. No. 2e-17;
Matches 39; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 8 PVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWQDSMDHL 67
DB 28 PSACCFRVTNKKISFQRLKSYKIITSSKCPQTAVIFEIKPDKMICADPKKKWQDAKKYL 87

QY 68 DKQQTQPK 75
DB 88 DQISQTTK 95

RESULT 15
JC2478
eotaxin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 16-Jul-1999
C:Accession: JC2478
R:Jose, P.J.; Adcock, I.M.; Griffiths-Johnson, D.A.; Berkman, N.; Wells, T.N.C.; William
Biochem. Biophys. Res. Commun. 205, 788-794, 1994
A:Title: Eotaxin: Cloning of an eosinophil chemoattractant cytokine and increased mRNA e
A:Reference number: JC2478; MUID:95091818; PMID:7999113
A:Accession: JC2478
A:Molecule type: mRNA
A:Residues: 1-96 <JOS>
A:Cross-references: EMBL:X77603; NID:g602551; PIDN:CAA54698.1; PID:g602552
C:Comment: This protein is identified as a potent eosinophil chemoattractant.
C:Superfamily: macrophage inflammatory protein
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-96/Product: eotaxin #status predicted <MAT>
F:93/Binding site: carbohydrate (Thr) (covalent) #status predicted

Query Match 51.1%; Score 207; DB 2; Length 96;
Best Local Similarity 55.9%; Pred. No. 1.3e-16;
Matches 38; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 8 PVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWQDSMDHL 67
DB 28 PSACCFRVTNKKISFQRLKSYKIITSSKCPQTAVIFEIKPDKMICADPKKKWQDAKKYL 87

QY 68 DKQQTQPK 75
DB 88 GQISQTTK 95

Search completed: August 30, 2004, 17:08:02
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 17:02:47 ; Search time 32 Seconds
(without alignments)
122.612 Million cell updates/sec

Title: 07330446.PEP

Perfect score: 405
Sequence: 1 cpdaiapvcyfntrki.....qkvvqdsmdhldkqtqpk 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 405 | 100.0 | 76 | 2 | US-08-716-188-2 |
| 2 | 405 | 100.0 | 76 | 2 | US-08-615-232A-5 |
| 3 | 405 | 100.0 | 76 | 3 | US-08-470-323-5 |
| 4 | 405 | 100.0 | 76 | 4 | US-09-195-457-5 |
| 5 | 405 | 100.0 | 76 | 4 | US-09-291-038-5 |
| 6 | 405 | 100.0 | 78 | 1 | US-08-330-163-12 |
| 7 | 405 | 100.0 | 78 | 1 | US-08-482-111-12 |
| 8 | 405 | 100.0 | 99 | 1 | US-08-127-499A-35 |
| 9 | 405 | 100.0 | 99 | 1 | US-08-482-847-35 |
| 10 | 405 | 100.0 | 99 | 1 | US-08-347-492B-8 |
| 11 | 405 | 100.0 | 99 | 1 | US-08-480-449-19 |
| 12 | 405 | 100.0 | 99 | 2 | US-08-479-126B-5 |
| 13 | 405 | 100.0 | 99 | 2 | US-08-421-144A-5 |
| 14 | 405 | 100.0 | 99 | 2 | US-08-726-830A-5 |
| 15 | 405 | 100.0 | 99 | 2 | US-08-660-542-19 |
| 16 | 405 | 100.0 | 99 | 2 | US-08-798-143-8 |
| 17 | 405 | 100.0 | 99 | 3 | US-07-927-391-24 |
| 18 | 405 | 100.0 | 99 | 3 | US-08-995-156A-5 |
| 19 | 405 | 100.0 | 99 | 3 | US-09-044-856A-5 |
| 20 | 405 | 100.0 | 99 | 3 | US-09-044-855A-5 |
| 21 | 405 | 100.0 | 99 | 4 | US-08-679-493A-152 |
| 22 | 405 | 100.0 | 99 | 4 | US-08-479-603-19 |
| 23 | 405 | 100.0 | 99 | 4 | US-09-419-281-5 |
| 24 | 405 | 100.0 | 99 | 4 | US-09-366-887A-10 |
| 25 | 405 | 100.0 | 99 | 4 | US-08-339-107-19 |
| 26 | 405 | 100.0 | 99 | 4 | US-09-545-894-5 |
| 27 | 405 | 100.0 | 99 | 5 | PCT-US96-10087-5 |

28 405 100.0 99 6 5212073-2
29 400 98.8 76 1 US-07-956-862A-1
30 400 98.8 76 1 US-08-250-958-1
31 400 98.8 76 1 US-08-235-659-1
32 400 98.8 78 5 PCT-US95-00605-1
33 362 89.4 68 4 US-09-463-458A-30
34 362 89.4 69 4 US-09-463-458A-31
35 362 89.4 69 4 US-09-463-458A-32
36 358 88.4 68 4 US-09-463-458A-9
37 358 88.4 68 4 US-09-463-458A-26
38 358 88.4 68 4 US-09-463-458A-29
39 315 77.8 99 3 US-09-133-521-5
40 287 70.9 76 3 US-08-613-822-19
41 287 70.9 76 4 US-09-479-729B-19
42 287 70.9 76 4 US-09-717-209-19
43 287 70.9 99 1 US-08-460-449-18
44 287 70.9 99 2 US-08-660-542-18
45 287 70.9 99 3 US-08-613-822-18

ALIGNMENTS

RESULT 1
US-08-716-188-2
; Sequence 2, Application US/08716188
; Patent No. 5908829
; GENERAL INFORMATION:
; APPLICANT: KELLY, RODNEY W
; TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF
; TITLE OF INVENTION: THE CERVIX
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/716,188
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/00733
; FILING DATE: 31-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9406463.1
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-188-2

Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Handwritten: MSCP-1 +
Handwritten: contract + agent

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 2

US-08-615-232A-5
; Sequence 5, Application US/08615232A
; Patent No. 5993814
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9318984
; FILING DATE: 14-SEP-1993

; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-615-232A-5

Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 3

US-08-470-323-5

; Sequence 5, Application US/08470323A
; Patent No. 6031080
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/08/470,323A
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: PCT/GB94/02006
; EARLIER FILING DATE: 1994-09-14
; EARLIER APPLICATION NUMBER: GB 9318984.3
; EARLIER FILING DATE: 1993-09-14
; EARLIER APPLICATION NUMBER: GB 94086902.2
; EARLIER FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-08-470-323-5

Query Match 100.0%; Score 405; DB 3; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 4

US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. 6605702
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.

; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195,457
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9318984.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-09-195-457-5

Query Match 100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,111
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fasse, J. Peter
/ REGISTRATION NUMBER: 32,983
/ REFERENCE/DOCKET NUMBER: 00231/083001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 78 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-482-111-12

Query Match 100.0%; Score 405; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 6.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 3 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62

Qy 61 QDSMDHLDKQOTPKT 76
Db 63 QDSMDHLDKQOTPKT 78

RESULT 8
US-08-127-499A-35
Sequence 35, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-127-499A-35

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

Qy 61 QDSMDHLDKQOTPKT 76
Db 84 QDSMDHLDKQOTPKT 99

RESULT 9
US-08-482-847-35
Sequence 35, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-482-847-35

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

Qy 61 QDSMDHLDKQOTPKT 76
Db 84 QDSMDHLDKQOTPKT 99

Epitope

Ab

RESULT 10

US-08-347-492B-8
; Sequence 8, Application US/08347492B
; Patent No. 5602008
; GENERAL INFORMATION:
; APPLICANT: Wilde, Craig G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
; PRODUCTION AND USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,492B
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PP-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 487124

US-08-347-492B-8
Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OPDAINAPVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
Qy 61 QDSMDHLDKQTQTPKT 76
Db 84 QDSMDHLDKQTQTPKT 99

RESULT 11

US-08-480-449-19
; Sequence 19, Application US/08480449
; Patent No. 5688927
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
; NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,449
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/32779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "Hu MCP-1"

US-08-480-449-19
Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OPDAINAPVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
Qy 61 QDSMDHLDKQTQTPKT 76
Db 84 QDSMDHLDKQTQTPKT 99

RESULT 12
US-08-479-126B-5
; Sequence 5, Application US/08479126B
; Patent No. 5866373
; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; APPLICANT: RUBEN, STEVEN M
; APPLICANT: SUTTON, GRANGER G III
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN MONOCYTE
; TITLE OF INVENTION: CHEMOTACTIC PROTEIN-4 (AS AMENDED)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

DNA

Handwritten signature/initials.

Handwritten signature/initials.

APPLICATION NUMBER: US/08/479,126B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340001
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-126B-5

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTPTKT 76
Db 84 QDSMDHLDKQTPTKT 99

RESULT 13
US-08-421-144A-5
Sequence 5, Application US/08421144A
Patent No. 5874211
GENERAL INFORMATION:
APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: STUART, SUSAN G.
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,144A
FILING DATE: 13-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0031 US
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-421-144A-5

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTPTKT 76
Db 84 QDSMDHLDKQTPTKT 99

RESULT 14
US-08-726-830A-5
Sequence 5, Application US/08726830A
Patent No. 5880263
GENERAL INFORMATION:
APPLICANT: LI HAODONG
APPLICANT: RUBEN, STEVEN M
APPLICANT: SUTTON, GRANGER G III
TITLE OF INVENTION: MONOCYTE CHEMOTACTIC PROTEIN-4
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,830A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,126
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340002
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-726-830A-5

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCVNFNTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCVNFNTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
Qy 61 QDSMDHLDKQTQTPKT 76
Db 84 QDSMDHLDKQTQTPKT 99

Db 84 QDSMDHLDKQTQTPKT 99
Search completed: August 30, 2004, 17:08:40
Job time : 35 secs

RESULT 15
US-08-660-542-19
; Sequence 19, Application US/08660542
; Patent No. 5932703
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,542
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,658
; FILING DATE: 16-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,620
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/33318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "Hu MCP-1"
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..76
; US-08-660-542-19

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QPDAINAPVTCVNFNTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCVNFNTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
Qy 61 QDSMDHLDKQTQTPKT 76

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 16:51:56 ; Search time 122 Seconds

(without alignments)
176.013 Million cell updates/sec

Title: 07330446.PBP

Perfect score: 405

Sequence: 1 gpdaipavtcycynftnrki.....gkwvqdsmdhldkgtptp 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|-------------|
| 1 | 405 | 100.0 | 76 | 2 AAR28660 | MCF. 3/20 |
| 2 | 405 | 100.0 | 76 | 2 AAR87680 | Monocyte |
| 3 | 405 | 100.0 | 76 | 3 AAY69030 | Amino aci |
| 4 | 405 | 100.0 | 76 | 5 AAO20010 | Human che |
| 5 | 405 | 100.0 | 76 | 5 AAO14143 | Human MCP |
| 6 | 405 | 100.0 | 76 | 5 AAM53048 | Human mon |
| 7 | 405 | 100.0 | 76 | 7 ADC89673 | Human mat |
| 8 | 405 | 100.0 | 76 | 7 ADD14998 | Human mon |
| 9 | 405 | 100.0 | 76 | 7 ADB80852 | huMCP1 ch |
| 10 | 405 | 100.0 | 76 | 7 ADS06777 | Human MCP |
| 11 | 405 | 100.0 | 99 | 1 AAP95387 | Human mon |
| 12 | 405 | 100.0 | 99 | 2 AAR28663 | MCF. 3/20 |
| 13 | 405 | 100.0 | 99 | 2 AAR73914 | Human mon |
| 14 | 405 | 100.0 | 99 | 2 AAR70800 | Chemocattr |
| 15 | 405 | 100.0 | 99 | 2 AAW40174 | Macrophag |
| 16 | 405 | 100.0 | 99 | 2 AAY26176 | Monocyte |
| 17 | 405 | 100.0 | 99 | 2 AAY48391 | Human pro |
| 18 | 405 | 100.0 | 99 | 3 AAS15785 | Human che |
| 19 | 405 | 100.0 | 99 | 4 AAB97914 | Human mon |
| 20 | 405 | 100.0 | 99 | 5 AAM52440 | HIV_Nef1 |
| 21 | 405 | 100.0 | 99 | 5 AAU77179 | Human sma |
| 22 | 405 | 100.0 | 99 | 5 ABB80901 | Human MCP |
| 23 | 405 | 100.0 | 99 | 5 ABP65214 | Hypoxia-r |
| 24 | 405 | 100.0 | 99 | 6 ABP96799 | Human COP |
| 25 | 405 | 100.0 | 99 | 7 ABU10502 | Human MCP |

| | | | | | |
|----|-----|-------|-----|------------|-----------|
| 26 | 405 | 100.0 | 99 | 7 ADC89670 | Human MCP |
| 27 | 405 | 100.0 | 99 | 8 ADE48100 | Human mon |
| 28 | 405 | 100.0 | 122 | 7 ADD14997 | Human mon |
| 29 | 405 | 100.0 | 325 | 3 AAY69049 | A chemokl |
| 30 | 405 | 100.0 | 327 | 3 AAY69050 | A chemokl |
| 31 | 405 | 100.0 | 332 | 3 AAY69051 | A chemokl |
| 32 | 402 | 99.3 | 76 | 2 AAW40175 | Macrophag |
| 33 | 402 | 99.3 | 76 | 3 AAS12818 | Human gli |
| 34 | 401 | 99.0 | 77 | 7 ADC89671 | Human MCP |
| 35 | 401 | 99.0 | 99 | 2 AAR06398 | Human MCP |
| 36 | 400 | 98.8 | 76 | 1 AAP90292 | Peptide f |
| 37 | 400 | 98.8 | 76 | 2 AAW09374 | Monocyte |
| 38 | 400 | 98.8 | 76 | 2 AAW11131 | Mature hu |
| 39 | 400 | 98.8 | 77 | 2 AAR86859 | Mature MC |
| 40 | 397 | 98.0 | 76 | 2 AAR87676 | (24-Arg) |
| 41 | 397 | 98.0 | 76 | 2 AAR87677 | (24-Arg) |
| 42 | 395 | 97.5 | 76 | 2 AAR87675 | (24-Arg) |
| 43 | 391 | 96.5 | 77 | 2 AAY14222 | Chemokine |
| 44 | 389 | 96.0 | 76 | 2 AAR53398 | Sense MCP |
| 45 | 389 | 96.0 | 77 | 7 ADC89672 | Human MCP |

ALIGNMENTS

RESULT 1

AAR28660
ID AAR28660 standard; protein; 76 AA.

XX AAR28660;

AC AC

25-MAR-2003 (revised)

24-MAR-1993 (first entry)

XX MCF.

DE MCF.

XX Plasmid; monocyte chemotactic factor; MCF; translation; termination;

KW terminator; initiation; ribosome binding site; RBS; promoter; tryptophan;

KW repressor.

XX Synthetic.

OS Synthetic.

XX WO9219737-A1.

XX 12-NOV-1992.

XX 27-APR-1992; 92WO-JP000550.

XX 09-MAY-1991; 91JP-00135950.

XX (DAIN) DAINIPPON PHARM CO LTD.

XX Yamagishi J, Matsuo N, Fukui T, Yamada M;

XX WPI; 1992-398864/48.

XX N-ESDB; AAQ30745, AAQ30746.

XX Prodn. of polypeptide(s) having monocyte-chemotactic activity - using

XX expression plasmids with E. coli elements and specific E.coli strains.

XX Claim 1; Page 48 + Page 36; 56pp; English.

XX An expression plasmid, pHM483, for producing MCF(76) consisting of 76

XX amino acids was constructed. The prod. can be used for e.g. treating

XX bacterial infectious diseases. (Updated on 25-MAR-2003 to correct FN

XX field.)

XX Sequence 76 AA;

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QY 1 OPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 2
 AAR87680
 ID AAR87680 standard; protein; 76 AA.
 AC AAR87680;
 XX
 DT 05-MAR-1996 (first entry)
 DE Monocyte chemotactic activating factor for use as wound remedy.
 KW monocyte chemotactic activating factor; MCPAF; wound remedy.
 XX Homo sapiens.
 OS
 PN WO9507710-A1.
 XX
 PD 23-MAR-1995.
 XX
 PP 13-SEP-1994; 94WO-TP001512.
 XX
 PR 13-SEP-1993; 93JP-00227385.
 XX
 PA (TORA) TORAY IND INC.
 XX
 PI Matsushima K, Naruto M;
 XX
 DR WPI; 1995-131181/17.
 XX
 PT Wound treatment using monocyte chemotactic factor - has potent
 PT therapeutic effect on skin wounds and ulcers.
 XX
 PS Disclosure; Page 12; 22pp; Japanese.
 XX
 CC The invention relates to a new remedy for curing wounds which, instead of
 CC comprising a growth factor, comprises a monocyte chemotactic activating
 CC factor (MCPAF) or its variants or derivatives. The factor has potent
 CC effect on skin wounds and ulcers. The present sequence is human MCPAF, the
 CC activity of which is exemplified as the new remedy
 XX
 SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 3
 AAY69030
 ID AAY69030 standard; protein; 76 AA.
 AC AAY69030;
 XX
 DT 30-MAY-2000 (first entry)
 DE Amino acid sequence of chemokine receptor ligand MCP-1.
 XX
 XX Human chemokine MCP-1 protein.
 XX Human; chemokine; anti-HIV; antiasthmatic; antiarthritic; antirheumatic;
 KW antiarteriosclerotic; dermatological; antiinflammatory; anti-allergic;
 KW

KW Chemokine receptor; ligand; inflammatory response; immune effector cell;
 KW secondary tissue damage; central nervous system injury; MCP-1;
 KW CNS inflammatory disease; neurodegenerative disorder; heart disease;
 KW inflammatory eye disease; inflammatory bowel disease;
 KW inflammatory joint disease; inflammatory kidney; renal disease;
 KW inflammatory lung disease; inflammatory nasal disease;
 KW inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200004926-A2.
 XX
 PD 03-FEB-2000.
 XX
 PP 21-JUL-1999; 99WO-CA000659.
 XX
 PR 22-JUL-1998; 98US-00120523.
 XX
 PA (OSPR-) OSPREY PHARM LTD.
 XX
 PI McDonald JR, Coggins PJ;
 XX
 DR WPI; 2000-182542/16.
 XX
 PT A new therapeutic agent comprising a conjugate for treating secondary
 PT tissue damage and other disease conditions like Alzheimer's disease,
 PT stroke, Parkinson's disease and atherosclerosis.
 XX
 PS Disclosure; Page 60; 204pp; English.
 XX
 CC The present sequence represents a chemokine receptor ligand. The present
 CC ligand can be incorporated into the conjugates of the invention. The
 CC specification describes a conjugate, comprising a targeted agent and a
 CC chemokine receptor ligand. The conjugate binds to a chemokine receptor
 CC resulting in internalisation of the targeted agent in cells bearing the
 CC receptor. The conjugates are used for formulating a medicament or for
 CC treating disorders associated with inflammatory responses resulting from
 CC activation, proliferation and migration of immune effector cells. The
 CC disorders or disease states comprise secondary tissue damage such as
 CC central nervous system (CNS) injury, CNS inflammatory diseases,
 CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
 CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
 CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal
 CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-
 CC regulated cancers
 XX
 SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 3; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 4
 AAO20010
 ID AAO20010 standard; protein; 76 AA.
 XX
 AC AAO20010;
 XX
 DT 11-JUN-2002 (first entry)
 DE Human chemokine MCP-1 protein.
 XX
 XX Human; chemokine; anti-HIV; antiasthmatic; antiarthritic; antirheumatic;
 KW antiarteriosclerotic; dermatological; antiinflammatory; anti-allergic;
 KW

immunosuppressive; polymer-modified bioactive synthetic chemokine; HIV; AIDS; asthma; allergic rhinitis; atopic dermatitis; rheumatoid arthritis; atheroma; atherosclerosis; organ transplant rejection; MCP-1.

Homo sapiens.

WO200204015-A1.

17-JAN-2002.

12-JUL-2001; 2001WO-US021933.

12-JUL-2000; 2000US-0217683P.

(GRYP-) GRYPHON SCI.

Kochendoerfer G, Botti P, Bradburne JA, Chen S, Cressman S;

WPI; 2002-268857/31.

New polymer-modified bioactive synthetic chemokines useful in the treatment of various diseases or disorders e.g. asthma.

Claim 8; Fig 10A; 176pp; English.

The invention relates to polymer-modified bioactive synthetic chemokines and to methods for their production and use. The compounds and methods of the backbone of the invention are useful in the analysis and treatment of various diseases states e.g. HIV and AIDS related disorders, asthma, allergic rhinitis, atopic dermatitis, atheroma/atherosclerosis, organ transplant rejection, and rheumatoid arthritis. This sequence represents the human chemokine MCP-1 protein of the invention

Sequence 76 AA;

Query Match 100.0%; Score 405; DB 5; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 5
 ID AAO14143
 AC AAO14143; standard; protein; 76 AA.

25-APR-2002 (first entry)

Human MCP-1 protein.

Human; chemokine receptor modulator; chemokine; HIV infection; AIDS; asthma; allergic rhinitis; atopic dermatitis; atheroma; antiinflammatory; antiasthmatic; antiallergic; dermatological; antiarteriosclerotic; antirheumatic; antiarthritic; anti-HIV; immunosuppressive; MCP-1; atherosclerosis; organ transplant rejection; rheumatoid arthritis.

Homo sapiens.

WO200204499-A1.

17-JAN-2002.

12-JUL-2001; 2001WO-US021934.

12-JUL-2000; 2000US-0217683P.

(GRYP-) GRYPHON SCI.

Offord R, Gaertner H, Hartley O;

WPI; 2002-171703/22.

Chemokine receptor modulator useful for treating e.g. asthma, allergic rhinitis comprises a chemically modified carboxyl-terminus and/or amino terminus analogs.

Example 3; Fig 2; 86pp; English.

The present invention relates to chemokine receptor modulators, which comprise a chemokine polypeptide chain modified at N-terminus with an aliphatic chain and at least one amino acid derivatives and/or modified at its C-terminus with an aliphatic chain or polycyclic. The modulators can be used to treat diseases such as HIV infection, AIDS, asthma, allergic rhinitis, atopic dermatitis, atheroma, atherosclerosis, organ transplant rejection and rheumatoid arthritis. The present sequence is the human MCP-1 protein

Sequence 76 AA;

Query Match 100.0%; Score 405; DB 5; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 6
 ID AAM53048
 AC AAM53048; standard; protein; 76 AA.

26-MAR-2002 (first entry)

Human monocyte chemoattractant protein-1 (MCP-1).

Human; monocyte chemoattractant protein-1; MCP-1; C-C chemokine family; pulmonary hypertension; primary; hypotensive.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 2..8 /note= "These residues are deleted in a specifically claimed human MCP-1 mutant, 7ND-MCP-1 (AAM53049)"

WO200189582-A1.

29-NOV-2001.

25-MAY-2001; 2001WO-JP004381.

26-MAY-2000; 2000JP-00161145.

(TAKE) TAKEDA CHEM IND LTD.
 (EGAS/) EGASHIRA K.

Egashira K, Yonemitsu Y, Sueishi K, Ikeda Y, Inada Y;

WPI; 2002-083059/11.

N-PSDB; ABA02497.

CC formation of fibrous capsules around the device. This is the amino acid
 CC sequence of human monocyte chemoattractant protein-1 (MCP-1) mature
 CC protein.
 XX
 SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 9

ADE80852
 ID ADE80852 standard; peptide; 76 AA.

AC ADE80852;

DT 29-JAN-2004 (first entry)

DE huMCP1 chemokine.

KW Nuclear targeting peptide; nuclear targeting domain; Eskine; PESKY;
 KW chemokine; cancer; cytostatic; huMCP1; chemokine.

XX Unidentified.

XX WO2003082920-A1.

XX 09-OCT-2003.

XX 02-APR-2003; 2003WO-GB001472.

XX 02-APR-2002; 2002GB-00007624.

XX (CANC-) CANCER RES TECHNOLOGY LTD.

XX Graham G;

XX WPI; 2003-788341/74.

DR New nuclear targeting peptide comprising a nuclear targeting domain
 PT isolated from a chemokine, useful for preparing a medicament for treating
 PT cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma.

XX Disclosure; Fig 11; 66pp; English.

XX The present invention relates to a nuclear targeting peptide (ADE80826)
 CC comprising a nuclear targeting domain isolated from the C-terminal
 CC sequence of the Eskine and PESKY chemokines. The nuclear targeting domain
 CC allows the protein to translocate to the cell nucleus. The nuclear
 CC targeting peptide is useful in preparing a medicament for treating
 CC cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma. The
 CC present sequence is a chemokine sequence, used in a sequence alignment in
 CC the invention.

SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 10

ADE06777
 ID ADE06777 standard; protein; 76 AA.

XX ADE06777;

XX 29-JAN-2004 (first entry)

DT Human MCP-1 SEQ ID NO:1.

DE human; MCP-1; monocyte chemoattractant protein-1; immunosuppressive;
 KW cardiant; neuroprotective; antimicrobial; cytostatic; gene therapy;
 KW immune disorder; cardiovascular disorder; neurological disorder;
 KW infectious disorder; malignant disorder.

XX Homo sapiens.

XX WO2003083059-A2.

XX 09-OCT-2003.

XX 24-MAR-2003; 2003WO-US009056.

XX 26-MAR-2002; 2002US-0367932P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Das A;

XX WPI; 2003-804039/75.

DR New monocyte chemoattractant protein-1 (MCP-1) mutein nucleic acid,
 PT useful for diagnosing or treating a MCP-1 mutein-related condition, e.g.
 PT immune, cardiovascular, neurologic or infectious or malignant disorders.

XX Claim 1; SEQ ID NO 1; 81pp; English.

XX The invention relates to a novel monocyte chemoattractant protein-1 (MCP-
 CC 1) mutant nucleic acid. A protein of the invention has immunosuppressive,
 CC cardiant, neuroprotective, antimicrobial, and cytostatic activity. A
 CC polynucleotide of the invention may have a use in gene therapy. The
 CC protein, nucleic acid, composition and method are useful for diagnosing
 CC or treating a MCP-1 mutein-related condition, e.g. immune,
 CC cardiovascular, neurologic or infectious or malignant disorders. The
 CC present sequence represents human MCP-1.

SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76

DB 61 QDSMDHLDKQTQTPKT 76

RESULT 11

AAP95387
 ID AAP95387 standard; protein; 99 AA.

XX AAP95387;

XX 25-MAR-2003 (revised)

PF 28-SEP-1994; 94WO-CA000516.
XX
PR 28-SEP-1993; 93US-00127499.
XX
PA (VALS/) VAN ALSTYNE D.
PA (SHAR/) SHARMA L R.
XX
XX
PI Van Alstyne D, Sharma LR;
XX
XX WPI; 1995-147431/19.
DR
XX
XX New peptide(s) and corresp. antibodies for the treatment of meningitis -
PT the peptide(s) corresp. to homologous antigenic sites on bacterial and
PT viral agents and on chemokine(s), used for detecting and preventing
PT meningitis.
XX
XX
PS Claim 47; Fig 8/10; 98pp; English.
XX
XX AAR73914 is the chemokine Human monocyte chemoattractant factor hMCP-1.
CC It contains the meningitis related antigenic sequences (MRHAS) claimed in
CC AAR73895 and AAR73907, which are recognised by a monoclonal antibody from
CC the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be
CC used in immunoassays to diagnose the presence of bacterial and/or viral
CC meningitis agents in a sample, or in prophylactic and therapeutic
CC meningitis treatments. The peptides may also be used as vaccines against
CC meningitis. NB: Identified by matching corresponding MRHAS peptides.
CC (Updated on 25-MAR-2003 to correct FN field.)
XX
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 14
AAR70800
ID AAR70800 standard; protein; 99 AA.
XX
AC AAR70800;
XX
XX 25-MAR-2003 (revised)
DT 29-AUG-1995 (first entry)
XX
XX Chemoattractant protein MCP-1.
XX
XX MCP-1; chemoattractant; heparanase; heparin; heparan sulfate; arthritis;
XX restenosis; cancer; wound healing.
XX
XX Homo sapiens.
XX
XX WO9504158-A1.
XX
XX 09-FEB-1995.
XX
XX 26-JUL-1994; 94WO-US008207.
XX
XX 29-JUL-1993; 93US-00099866.
PR 13-OCT-1993; 93US-00136117.
XX
XX (UPJO) UPJOHN CO.
XX
XX Hoogwerf AJ, Ledbetter SR;
XX
XX WPI; 1995-082239/11.
DR

DR N-PSDB; AAQ85370.
XX
PT Screening for cpds. with anti-heparanase activity - by detecting
PT inhibition of heparin or heparan sulphate degradation, potentially useful
PT for treating arthritis, restenosis, cancer.
XX
XX
PS Claim 13; Page 49; 60pp; English.
XX
XX Purified heparanases, prepared under reducing conditions and activated
CC with transglutaminase, are given in AAR70786-804. Most are prepared by
CC reverse transcription of mRNA from activated human leukocytes, then
CC cloning of the cDNA into pVL1392 baculovirus vector, and expression in
CC Sf9 cells in the presence of reduced glutathione and dithiothreitol.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 15
AAR70800
ID AAR70800 standard; protein; 99 AA.
XX
AC AAR70800;
XX
XX 01-JUL-1998 (first entry)
DT
XX
XX Macrophage chemoattractant peptide designated MCP-1.
XX
XX Monocyte chemoattractant peptide; MCP; MCP-1; treatment; neoplasm;
XX infection; human; monocyte receptor; chemotactic response; inflammation;
XX monocyte infiltration.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH FT Modified-site 37..39 /note= "potential N-linked glycosylation site"
XX
XX US5714578-A.
XX
XX 03-FEB-1998.
XX
XX 06-JUN-1995; 95US-00466280.
XX
XX 31-JAN-1989; 89US-00304234.
PR 30-MAR-1989; 89US-00330446.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Leonard EJ, Appella E, Robinson EA, Yoshimura T;
XX WPI; 1998-129909/12.
DR N-PSDB; AAV10341.
XX
XX Peptide with chemotactic activity for monocytes - from human monocytes or
PT glioma cells, useful for treating infections and neoplasms.
XX
XX Disclosure; Fig 2; 21pp; English.
XX
XX The present sequence represents a monocyte chemoattractant peptide (MCP)
CC designated MCP-1. MCPs can be isolated from human glioma cell line U-

CC 105MG and peripheral blood mononuclear leukocytes. MCPs are used for the
CC treatment of neoplasms and infections in humans. Short peptides derived
CC from MCPs can be screened to identify those that can bind to the monocyte
CC receptor without stimulating a chemotactic response. These are
CC potentially useful for treating inflammation associated with monocyte
CC infiltration
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDALNAPVTCYNTNPKISVQRLASVRRITSSKCPKEAVIFKTIIVAKIICADPKQKW 60
DB 24 QPDALNAPVTCYNTNPKISVQRLASVRRITSSKCPKEAVIFKTIIVAKIICADPKQKW 83
QY 61 QDSMDHLDKQTTPKT 76
DB 84 QDSMDHLDKQTTPKT 99

Search completed: August 30, 2004, 17:04:49
Job time : 126 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: August 30, 2004, 17:07:28 ; Search time 129 Seconds
(without alignments)
195.353 Million cell updates/sec
Title: 07330446.PEP
Perfect score: 405
Sequence: 1 qpdaainapvtccynftnrki.....qkwvqdamdhldkgtptkt 76
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1297172 seqs, 314612898 residues
Total number of hits satisfying chosen parameters: 1297172
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pap:
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pap:
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pap:
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pap:
6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pap:
7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pap:
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pap:
9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pap:
10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pap:
11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pap:
12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pap:
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pap:
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pap:
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pap:
16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pap:
17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pap:
18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pap:

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 405 | 100.0 | 76 | 9 | US-09-195-457-5 |
| 2 | 405 | 100.0 | 76 | 9 | US-09-792-793A-20 |
| 3 | 405 | 100.0 | 76 | 14 | US-10-339-778-3 |
| 4 | 405 | 100.0 | 76 | 14 | US-10-276-971-1 |
| 5 | 405 | 100.0 | 76 | 15 | US-10-375-209A-20 |
| 6 | 405 | 100.0 | 76 | 16 | US-10-332-038A-5 |
| 7 | 405 | 100.0 | 76 | 16 | US-10-668-733-7 |
| 8 | 405 | 100.0 | 76 | 16 | US-10-668-733-14 |
| 9 | 405 | 100.0 | 78 | 16 | US-10-803-960-14 |
| 10 | 405 | 100.0 | 99 | 12 | US-10-449-831A-210 |
| 11 | 405 | 100.0 | 99 | 8 | US-09-927-939-16 |
| 12 | 405 | 100.0 | 99 | 10 | US-09-920-137A-9 |
| 13 | 405 | 100.0 | 99 | 12 | US-10-054-967-5 |
| 14 | 405 | 100.0 | 99 | 12 | US-10-385-395 |
| 15 | 405 | 100.0 | 99 | 13 | US-10-057-275-9 |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 405 | 100.0 | 76 | 9 | US-09-195-457-5 |
| 2 | 405 | 100.0 | 76 | 9 | US-09-792-793A-20 |
| 3 | 405 | 100.0 | 76 | 14 | US-10-339-778-3 |
| 4 | 405 | 100.0 | 76 | 14 | US-10-276-971-1 |
| 5 | 405 | 100.0 | 76 | 15 | US-10-375-209A-20 |
| 6 | 405 | 100.0 | 76 | 16 | US-10-332-038A-5 |
| 7 | 405 | 100.0 | 76 | 16 | US-10-668-733-7 |
| 8 | 405 | 100.0 | 76 | 16 | US-10-668-733-14 |
| 9 | 405 | 100.0 | 78 | 16 | US-10-803-960-14 |
| 10 | 405 | 100.0 | 99 | 12 | US-10-449-831A-210 |
| 11 | 405 | 100.0 | 99 | 8 | US-09-927-939-16 |
| 12 | 405 | 100.0 | 99 | 10 | US-09-920-137A-9 |
| 13 | 405 | 100.0 | 99 | 12 | US-10-054-967-5 |
| 14 | 405 | 100.0 | 99 | 12 | US-10-385-395 |
| 15 | 405 | 100.0 | 99 | 13 | US-10-057-275-9 |

US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. US20020081623A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195,457
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9319984.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-09-195-457-5

ALIGNMENTS

| | | | | | |
|----|-----|-------|-----|----|----------------------|
| 16 | 405 | 100.0 | 99 | 13 | US-10-033-067-4 |
| 17 | 405 | 100.0 | 99 | 13 | US-10-141-965-5 |
| 18 | 405 | 100.0 | 99 | 14 | US-10-146-496-9 |
| 19 | 405 | 100.0 | 99 | 14 | US-10-293-705-8 |
| 20 | 405 | 100.0 | 99 | 14 | US-10-137-655-9 |
| 21 | 405 | 100.0 | 99 | 15 | US-10-116-275-222 |
| 22 | 405 | 100.0 | 99 | 15 | US-10-440-464-62 |
| 23 | 405 | 100.0 | 99 | 16 | US-10-764-649-18 |
| 24 | 405 | 100.0 | 122 | 14 | US-10-339-778-2 |
| 25 | 405 | 100.0 | 122 | 14 | US-10-339-778-2 |
| 26 | 405 | 100.0 | 133 | 12 | US-10-449-831A-214 |
| 27 | 405 | 100.0 | 325 | 9 | US-09-792-793A-71 |
| 28 | 405 | 100.0 | 325 | 15 | US-10-375-209A-71 |
| 29 | 405 | 100.0 | 327 | 9 | US-09-792-793A-72 |
| 30 | 405 | 100.0 | 327 | 15 | US-10-375-209A-72 |
| 31 | 405 | 100.0 | 332 | 9 | US-09-792-793A-73 |
| 32 | 398 | 98.3 | 332 | 15 | US-10-375-209A-73 |
| 33 | 398 | 98.3 | 99 | 9 | US-09-834-795A-28 |
| 34 | 362 | 89.4 | 99 | 10 | US-09-834-794A-28 |
| 35 | 362 | 89.4 | 69 | 14 | US-10-339-778-4 |
| 36 | 357 | 88.1 | 69 | 14 | US-10-276-971-2 |
| 37 | 293 | 72.3 | 90 | 12 | US-10-424-599-263303 |
| 38 | 293 | 72.3 | 97 | 10 | US-09-920-137A-5 |
| 39 | 293 | 72.3 | 97 | 13 | US-10-057-275-5 |
| 40 | 287 | 70.9 | 97 | 14 | US-10-137-655-5 |
| 41 | 287 | 70.9 | 76 | 9 | US-09-792-793A-22 |
| 42 | 287 | 70.9 | 76 | 12 | US-10-646-770-19 |
| 43 | 287 | 70.9 | 76 | 14 | US-10-125-451-19 |
| 44 | 287 | 70.9 | 76 | 14 | US-10-263-139-19 |
| 45 | 287 | 70.9 | 76 | 15 | US-10-375-209A-22 |
| | | | 76 | 16 | US-10-332-038A-6 |

RESULT 1
US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. US20020081623A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195,457
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9319984.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-09-195-457-5

Query Match 100.0%; Score 405; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1 | QPDAINAPVTCCYNFTNRKISVORLASYPRTSSKCPKEAVIFKTTVAKEICADPKQKWV | 60 |
| Db | 1 | QPDAINAPVTCCYNFTNRKISVORLASYPRTSSKCPKEAVIFKTTVAKEICADPKQKWV | 60 |
| Qy | 61 | QDSWDHLDKOTQPKT | 76 |

Db 61 QDSMDHLKQTQTPKT 76

RESULT 2
US-09-792-793A-20
; Sequence 20, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-09-792-793A-20

Query Match 100.0%; Score 405; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLKQTQTPKT 76
Db 61 QDSMDHLKQTQTPKT 76

RESULT 3
US-10-339-778-3
; Sequence 3, Application US/10339778
; Publication No. US20030129214A1
; GENERAL INFORMATION:
; APPLICANT: Bornstein, P.
; APPLICANT: Kyriakides, T.
; TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDIC
; TITLE OF INVENTION: DEVICE
; FILE REFERENCE: UNOTL-1-20275
; CURRENT APPLICATION NUMBER: US/10/339,778
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,560
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 3
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-339-778-3

Query Match 100.0%; Score 405; DB 14; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLKQTQTPKT 76
Db 61 QDSMDHLKQTQTPKT 76

RESULT 4
US-10-276-971-1
; Sequence 1, Application US/10276971
; Publication No. US20030162737A1
; GENERAL INFORMATION:
; APPLICANT: Egashira Kensuke
; APPLICANT: Yoshikazu Yonemitsu
; APPLICANT: Katsuo Sueishi
; APPLICANT: Yasuhiro Ikeda
; APPLICANT: Yoshiyuki Inada
; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
; FILE REFERENCE: 2733 USOP
; CURRENT APPLICATION NUMBER: US/10/276,971
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Human
US-10-276-971-1

Query Match 100.0%; Score 405; DB 14; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLKQTQTPKT 76
Db 61 QDSMDHLKQTQTPKT 76

RESULT 5
US-10-375-209A-20
; Sequence 20, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-10-375-209A-20

Query Match 100.0%; Score 405; DB 15; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 QDSMDHLKQTQTPKT 76
Db 61 QDSMDHLKQTQTPKT 76

RESULT 6
US-10-332-038A-5
; Sequence 5, Application US/10332038A
; Publication No. US20040077835A1


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; GENERAL INFORMATION:
; APPLICANT: Gryphon Therapeutics, Inc.
; APPLICANT: Offord, Robin
; APPLICANT: Gaertner, Hubert
; APPLICANT: Hattley, Oliver
; TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use
; FILE REFERENCE: 03504.271
; CURRENT APPLICATION NUMBER: US/10/332,038A
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2002-09-23
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-332-038A-5

Query Match      100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
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QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 7
US-10-668-733-7
; Sequence 7, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT APPLICATION NUMBER: US/10/668,733
; PRIOR FILING DATE: 2003-09-23
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-668-733-7

Query Match      100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 8
US-10-668-733-14
; Sequence 14, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT APPLICATION NUMBER: US/10/668,733
; PRIOR FILING DATE: 2003-09-23
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 14
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-668-733-14

Query Match      100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 9
US-10-803-960-14
; Sequence 14, Application US/10803960
; Publication No. US20040156822A1
; GENERAL INFORMATION:
; APPLICANT: White, John R.
; APPLICANT: Pelus, Louis
; APPLICANT: Li, Haodong
; APPLICANT: Kreider, Brent L.
; TITLE OF INVENTION: Novel Chemokine for Mobilizing Stem Cells
; FILE REFERENCE: PF497D2
; CURRENT APPLICATION NUMBER: US/10/803,960
; PRIOR FILING DATE: 2004-03-19
; CURRENT APPLICATION NUMBER: 09/567,225
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/225,501
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/006,051
; PRIOR FILING DATE: 1995-10-24
; PRIOR APPLICATION NUMBER: US 08/740,033
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 78
; TYPE: PRT
; ORGANISM: MCP-1
US-10-803-960-14

Query Match      100.0%; Score 405; DB 16; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 3 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62

QY 61 QDSMDHLDKQTQTPKT 76
Db 63 QDSMDHLDKQTQTPKT 78

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RESULT 10

US-10-449-831A-210
; Sequence 210, Application US/10449831A
; Publication No. US20040029179A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; TITLE OF INVENTION: Higher molecular weight entities and uses therefor
; FILE REFERENCE: 2385978
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/10/449,831A
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human
US-10-449-831A-210

Query Match 100.0%; Score 405; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 6.2e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
DB 23 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 82
QY 61 QDSMDHLDKQTQTPKT 76
DB 83 QDSMDHLDKQTQTPKT 98

RESULT 11

US-08-927-939-16
; Sequence 16, Application US/08927939
; Publication No. US20010006640A1
; GENERAL INFORMATION:

; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295,022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11

; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens

US-08-927-939-16

Query Match 100.0%; Score 405; DB 8; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
DB 24 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 12

US-09-920-137A-9
; Sequence 9, Application US/09920137A
; Publication No. US20030049725A1
; GENERAL INFORMATION:

; APPLICANT: Coleman, Roger
; APPLICANT: Bandman, Olga
; APPLICANT: Wilde, Craig G.
; TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/920,137A

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954

REFERENCE/DOCKET NUMBER: PF-0027 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-852-0195

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 99 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: MCP-1

US-09-920-137A-9

Query Match 100.0%; Score 405; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
DB 24 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 13

US-10-054-967-5

; Sequence 5, Application US/10054967

; Publication No. US20030059874A1

; GENERAL INFORMATION:

; APPLICANT: KREIDER, BRENT L.

; RUBEN, STEVEN M.

; OLSEN, HENRIK S.

; TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS

; NUMBER OF SEQUENCES: 114

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,967
FILING DATE: 25-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/995,156
FILING DATE: 19-DEC-1997
APPLICATION NUMBER: 60/042,269
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-054-967-5

Query Match 100.0%; Score 405; DB 12; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 14

US-10-170-385-395
Sequence 395, Application US/10170385
Publication No. US20030203372A1
GENERAL INFORMATION:
APPLICANT: Ward, Neil Raymond
APPLICANT: Mundy, Christopher Robert
APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: White, Jonathan
APPLICANT: Binley, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Naylor, Stuart
APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 395
LENGTH: 99
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-170-385-395

Query Match 100.0%; Score 405; DB 12; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 15

US-10-057-275-9
Sequence 9, Application US/10057275
Publication No. US2002015545A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
Bandman, Olga
Wilde, Craig G.
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/057,275
FILING DATE: 25-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/390,740A
FILING DATE: February 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0027 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: MCP-1
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-057-275-9

Query Match 100.0%; Score 405; DB 13; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

Search completed: August 30, 2004, 17:19:01
Job time : 131 secs

Wed Sep 1 08:47:04 2004

07330446.pap.rapb

Page 6

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 16:52:21 ; Search time 24 Seconds
(without alignments)
164.889 Million cell updates/sec

Title: 07330446.PEP
Perfect score: 405
Sequence: 1 qpdainapvtccynftnrki.....qkwvqdsmdhldkgtqtpkt 76

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 405 | 100.0 | 99 | 1 SY02_HUMAN | P13500 homo sapien |
| 2 | 394 | 97.3 | 99 | 1 SY02_WACFA | Q9MYN4 macaca fasc |
| 3 | 394 | 83.2 | 99 | 1 SY02_PIG | P42831 sus scrofa |
| 4 | 331 | 81.7 | 101 | 1 SY02_CANFA | P52203 canis fami |
| 5 | 315 | 77.8 | 99 | 1 MCPA_BOVIN | P28291 bos taurus |
| 6 | 314 | 77.5 | 125 | 1 SY02_RABIT | P28292 oryctolagus |
| 7 | 308 | 76.0 | 74 | 1 MCPB_BOVIN | P80343 bos taurus |
| 8 | 287 | 70.9 | 99 | 1 SY07_HUMAN | P80098 homo sapien |
| 9 | 284 | 70.1 | 104 | 1 SY12_MOUSE | Q24401 mus musculu |
| 10 | 273 | 67.4 | 97 | 1 EOTA_HUMAN | P51671 homo sapien |
| 11 | 268 | 66.2 | 99 | 1 SY08_HUMAN | P80075 homo sapien |
| 12 | 261 | 64.4 | 99 | 1 SY08_PIG | P49873 sus scrofa |
| 13 | 253.5 | 62.6 | 98 | 1 SY13_HUMAN | Q99616 homo sapien |
| 14 | 252 | 62.2 | 148 | 1 SY02_MOUSE | P10148 mus musculu |
| 15 | 247 | 61.0 | 99 | 1 SY08_BOVIN | Q99141 bos taurus |
| 16 | 241 | 59.5 | 148 | 1 SY02_RAT | P48444 rattus norv |
| 17 | 236 | 59.3 | 120 | 1 SY02_CAVPO | Q08782 cavia porce |
| 18 | 221 | 54.6 | 97 | 1 EOTA_RAT | P97545 rattus norv |
| 19 | 218 | 53.8 | 97 | 1 EOTA_MOUSE | P48298 mus musculu |
| 20 | 214 | 52.8 | 96 | 1 EOTA_CAVPO | P80325 cavia porce |
| 21 | 205 | 50.6 | 97 | 1 SY07_MOUSE | Q03366 mus musculu |
| 22 | 202 | 49.9 | 97 | 1 SY07_RAT | Q9qxy8 rattus norv |
| 23 | 177 | 43.7 | 97 | 1 SY08_MOUSE | Q92121 mus musculu |
| 24 | 152 | 37.5 | 119 | 1 SY24_MOUSE | Q9jkc0 mus musculu |
| 25 | 148.5 | 36.7 | 70 | 1 REG1_BOVIN | P82943 bos taurus |
| 26 | 145.5 | 35.9 | 93 | 1 SY3L_HUMAN | P16619 homo sapien |
| 27 | 142.5 | 35.2 | 92 | 1 SY03_HUMAN | P10147 homo sapien |
| 28 | 137 | 33.8 | 119 | 1 SY24_HUMAN | O00175 homo sapien |
| 29 | 135.5 | 33.5 | 90 | 1 SY04_CHICK | Q90826 gallus gall |
| 30 | 133.5 | 33.5 | 92 | 1 SY04_HUMAN | P32336 h small ind |
| 31 | 133.5 | 33.0 | 92 | 1 SY04_RABIT | P46632 oryctolagus |
| 32 | 133.5 | 33.0 | 92 | 1 SY04_RAT | P50230 rattus norv |
| 33 | 131 | 32.3 | 393 | 1 SYD1_RAT | O55145 rattus norv |

ALIGNMENTS

RESULT 1

| SY02_HUMAN | SY02_HUMAN | STANDARD; | PRT; | 99 AA. |
|------------|--|-----------|------|--------|
| AC | P13500; Q9UDF3; | | | |
| DT | 01-JAN-1990 (Rel. 13, Created) | | | |
| DT | 01-JAN-1990 (Rel. 13, Last sequence update) | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |
| DE | Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein-1) (MCP-1) (Monocyte chemoattractant protein-1) (Monocyte chemoattractant and activating factor) (MCAF) (Monocyte secretory protein JE) (HC11). | | | |
| DE | CCL2 OR SCYA2 OR MCP1. | | | |
| GN | Homo sapiens (Human). | | | |
| OS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=89165862; PubMed=2923622; | | | |
| RA | Furutani Y., Nomura H., Notake M., Oyama Y., Fukui T., Yamada M., Larsen C.G., Oppenheim J.J., Matsushima K.; | | | |
| RA | "Cloning and sequencing of the cDNA for human monocyte chemoattractant protein-1 (MCP-1) (Monocyte chemoattractant and activating factor) (MCAF)."; | | | |
| RT | Cloning and sequencing of the cDNA for human monocyte chemoattractant protein-1 (MCP-1) (Monocyte chemoattractant and activating factor) (MCAF)."; | | | |
| RL | Biochem. Biophys. Res. Commun. 159:249-255(1989). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=90097880; PubMed=2513477; | | | |
| RA | Rollins B.J., Stier P., Ernst T., Wong G.G.; | | | |
| RA | "The human homolog of the JE gene encodes a monocyte secretory protein."; | | | |
| RT | Cloning and sequencing of the JE gene encodes a monocyte secretory protein."; | | | |
| RL | Mol. Cell. Biol. 9:4687-4695(1989). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=89153605; PubMed=2465924; | | | |
| RA | Yoshimura T., Yuhki N., Moore S.K., Appella E., Lerman M.I., Leonard E.J.; | | | |
| RA | "Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression in mitogen-stimulated blood mononuclear leukocytes, and sequence similarity to mouse competence gene JE."; | | | |
| RT | FEBS Lett. 244:487-493(1989). | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=90290456; PubMed=2357211; | | | |
| RA | Shyu Y.J., Li Y.S., Kolattukudy P.E.; | | | |
| RA | "Structure of human monocyte chemoattractant protein gene and its regulation by TPA."; | | | |
| RT | Regulation by TPA."; | | | |
| RL | Biochem. Biophys. Res. Commun. 169:346-351(1990). | | | |
| RN | [5] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=91207938; PubMed=2518726; | | | |
| RA | Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.; | | | |
| RA | "Cloning and expression of a gamma-interferon-inducible gene in monocytes: a new member of a cytokine gene family."; | | | |
| RT | Int. Immunol. 1:388-399(1989). | | | |
| RN | [6] | | | |
| RP | SEQUENCE FROM N.A. | | | |

lots of new

RT MEDLINE=94150478; PubMed=8107690;
RA Li Y.S., Shyy Y.J., Wright J.G., Valente A.J., Cornhill J.F.,
RA Kolattukudy P.E.;
RT "The expression of monocyte chemoattractant protein (MCP-1) in human
RT vascular endothelium in vitro and in vivo.";
RL Mol. Cell. Biochem. 126:61-68(1993).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=92095166; PubMed=1661560;
RA Yoshimura T., Leonard E.J.;
RT "Human monocyte chemoattractant protein-1 (MCP-1).";
RL Adv. Exp. Med. Biol. 305:47-56(1991).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=91301709; PubMed=2071154;
RA Rollins B.J., Morton C.C., Ledbetter D.H., Eddy R.L. Jr., Shows T.B.;
RT "Assignment of the human small inducible cytokine A2 gene, SCYA2
RT (encoding JE or MCP-1), to 17q11.2-12: evolutionary relatedness of
RT cytokines clustered at the same locus.";
RL Genomics 10:489-492(1991).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=20374005; PubMed=10918580;
RA Finzer P., Soto U., Dellus H., Patzelt A., Pouetka A., Coy J.F.,
RA zur Hausen H., Roess F.;
RT "Differential transcriptional regulation of the
RT monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and
RT non-tumorigenic HPV 18 positive cells: The role of the chromatin
RT structure and AP-1 composition.";
RL Oncogene 19:3235-3244(2000).
RN [10]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Haptschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heideh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP SEQUENCE OF 24-99.
RX MEDLINE=89184525; PubMed=2648385;
RA Robinson E.A., Yoshimura T., Leonard E.J., Tanaka S., Griffin P.R.,
RA Shabanowitz J., Hunt D.F., Appella E.;
RT "Complete amino acid sequence of a human monocyte chemoattractant, a
RT putative mediator of cellular immune reactions.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1850-1854(1989).
RN [13]
RP SEQUENCE OF 29-53 AND 82-92.
RX MEDLINE=90211336; PubMed=232286;
RA Decock B., Conings R., Lenaers J.-P., Billiau A., van Damme J.;
RT "Identification of the monocyte chemoattractant protein from human
RT osteosarcoma cells and monocytes: detection of a novel N-terminally
processed form.";
RL Biochem. Biophys. Res. Commun. 167:904-909(1990).
RN [14]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=91312872; PubMed=1857712;
RA Gronenborn A.M., Clore G.M.;
RT "Modeling the three-dimensional structure of the monocyte chemo-
RT attractant and activating protein MCP-1 on the basis of the
RT solution structure of interleukin-8.";
RL Protein Eng. 4:263-269(1991).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=97143315; PubMed=8989326;
RA Lubkowski J., Bujacz G., Domaille P.J., Handel T.M., Wlodawer A.;
RT "The structure of MCP-1 in two crystal forms provides a rare example
RT of variable quaternary interactions.";
RL Nat. Struct. Biol. 4:64-69(1997).
RN [16]
RP STRUCTURE BY NMR.
RX MEDLINE=96234959; PubMed=8639605;
RA Handel T.M., Domaille P.J.;
RT "Heteronuclear (1H, 13C, 15N) NMR assignments and solution structure
RT of the monocyte chemoattractant protein-1 (MCP-1) dimer.";
RL Biochemistry 35:6569-6584(1996).
RN [17]
RP EFFECT OF DELETION OF N-TERMINAL RESIDUES.
RX MEDLINE=96195223; PubMed=8627182;
RA Weber M., Ugucioni M., Baggioni M., Clark-Lewis I., Dahinden C.A.;
RT "Deletion of the NH2-terminal residue converts monocyte chemoattractant
RT protein 1 from an activator of basophil mediator release to an
RT eosinophil chemoattractant.";
RL J. Exp. Med. 183:681-685(1996).
RN [18]
RP MUTAGENESIS.
RX MEDLINE=94253189; PubMed=8195247;
RA Zhang Y.J., Rutledge B.J., Rollins B.J.;
RT "Structure/activity analysis of human monocyte chemoattractant
RT protein-1 (MCP-1) by mutagenesis. Identification of a mutated protein
RT that inhibits MCP-1-mediated monocyte chemotaxis.";
RL J. Biol. Chem. 269:15918-15924(1994).
RN [19]
RP SUBUNIT.
RX MEDLINE=97053697; PubMed=8898111;
RA Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte
RT chemoattractant protein-3.";
RL FEBS Lett. 395:277-282(1996).
CC -/- FUNCTION: Chemoattractant factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Augments monocyte anti-tumor
CC activity. Has been implicated in the pathogenesis of diseases
CC characterized by monocyte infiltrates, like psoriasis, rheumatoid
CC arthritis or atherosclerosis. May be involved in the recruitment
CC of monocytes into the arterial wall during the disease process of
CC atherosclerosis. Binds to CCR2 and CCR4.
CC -/- SUBUNIT: Monomer or homodimer; in equilibrium.
CC -/- SUBCELLULAR LOCATION: Secreted.
CC -/- PTM: PROCESSING AT THE N-TERMINUS CAN REGULATE RECEPTOR AND TARGET
CC CELL SELECTIVITY. DELETION OF THE N-TERMINAL RESIDUE CONVERTS
CC IT FROM AN ACTIVATOR OF BASOPHIL TO AN EOSINOPHIL CHEMOATTRACTANT.
CC -/- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC -----
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CC -----
DR EMBL; M31626; AAA36330.1; -
DR EMBL; M30816; AAA36330.1; JOINED.
DR EMBL; M31625; AAA36330.1; JOINED.
DR EMBL; M24545; AAA18164.1; -

```
Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETICADPKQKW 60
    |||
Db 24 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETICADPKQKW 83
    |||

QY 61 QDSMDHLDKQTQTPK 76
    |||
Db 84 QDSMDHLDKQTQTPK 99
    |||

RESULT 2
SY02_MACFA
ID SY02_MACFA STANDARD; PRT; 99 AA.
AC Q9WIN4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein-1) (MCP-1) (Monocyte chemoattractant protein-1).
DE CC2 OR SCYA2 OR MCP1.
GN Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541, 9544;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis;
RA Studer C., Ufer R.;
RT "Cloning and expression of cynomolgus monkey chemoattractant protein-1."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RA Studer C., Ufer R.;
RT "Cloning and expression of rhesus monkey monocyte chemoattractant protein-1."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemoattractant factor that attracts monocytes and basophils but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By similarity).
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
DR EMBL; AF276081; AAF61899.1; -
DR EMBL; AF255343; AAF67756.1; -
DR HSSP; P13500; 1DOK.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response;
KW Pyrolidone carboxylic acid.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A2.
```

```
FT MOD_RES 24 24 PYROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64EE7A4F CRC64;

Query Match 97.3%; Score 394; DB 1; Length 99;
Best Local Similarity 98.7%; Pred. No. 3e-39;
Matches 74; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETICADPKQKW 60
    |||
Db 24 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETICADPKQKW 83
    |||

QY 61 QDSMDHLDKQTQTPK 75
    |||
Db 84 QDSMDHLDKQTQTPK 98
    |||

RESULT 3
SY02_PIG
ID SY02_PIG STANDARD; PRT; 99 AA.
AC P42831;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein-1) (MCP-1) (MCP-1) (Monocyte chemoattractant protein-1).
DE CC2 OR SCYA2.
GN Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94183284; PubMed=7510952;
RA Hosang X., Knoke I., Klaudiny J., Wempe F., Wuttke W., Scheit K.H.;
RT "Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): analysis by polymerase chain reaction and cDNA cloning."
RL Biochem. Biophys. Res. Commun. 199;962-968(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Zach O.R.F.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemoattractant factor that attracts monocytes, but not neutrophils.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
DR EMBL; Z48479; CAA88370.1; -
DR EMBL; X79416; CAA55945.1; -
DR FIR; JC2136; JC2136.
DR HSSP; P13500; 1DOK.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response;
KW Pyrolidone carboxylic acid.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A2.
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FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 101 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 99 AA; 10976 MW; 4COAC6278D4FOA09 CRC64;

Query Match 83.2%; Score 337; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.4e-32; Indels 0; Gaps 0;
Matches 60; Conservative 8; Mismatches 7;

QY 1 QPDAINAPVTCYCNFTNRKISVQLASVRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 60
DB 24 QPDALNSPVTCCYTLTKSKISQRLMSYRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 83
QY 61 QDSMDHLDK--QTQPK 75
DB 84 QDSISHLDKKQOTPK 98

RESULT 4
SY02_CANPA STANDARD; PRT; 101 AA.
ID _SY02_CANPA
AC P52203;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
DE CCL2 OR SCYA2 OR MCP1.
GN Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Jugular vein endothelial;
RX MEDLINE=97176620; PubMed=9024159;
RA Kumar A.G., Ballantyne C.M., Michael L.H., Kukiela G.L., Youker K.A.,
RA Lindsey M.L., Hawkins H.K., Birdsell H.H., Mackay C.R., Larosa G.J.,
RA Rossen R.D., Smith C.W., Entman M.L.;
RT "Induction of monocyte chemoattractant protein-1 in the small veins
RT of the ischemic and reperfused canine myocardium."
RL Circulation 95:693-700(1997).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils. Important factor in the course of the inflammatory
CC reaction to reperfusion of the previously ischemic myocardium.
CC May play a significant role in monocyte trafficking into the
CC reperfused myocardium.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Endothelium of small veins and intrafascicular
CC veins, and infiltrating leukocytes.
CC -!- INDUCTION: By TNF-alpha.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC EMBL; U29653; AAA84911.1; -.
CC HSSP; P13500; 1DOM.
CC InterPro; IPR000827; CC_chemokine_sml.
CC InterPro; IPR001811; Chemokine IL8.
CC Pfam; PF00048; IL8; 1.
CC PRINTS; PR01721; FRCTALKINE.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC Cytokine; Chemotaxis; Signal; Inflammatory response;

KW Pyrolidone carboxylic acid.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 101 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11121 MW; CDD7E2B1901A7267 CRC64;

Query Match 81.7%; Score 331; DB 1; Length 101;
Best Local Similarity 80.5%; Pred. No. 7e-32; Indels 2; Gaps 1;
Matches 62; Conservative 7; Mismatches 5;

QY 1 QPDAINAPVTCYCNFTNRKISVQLASVRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 60
DB 24 QPDALISPTCCYTLTKKISQRLMSYRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 83
QY 61 QDSMDHLDK--QTQPK 75
DB 84 QDSMAHLDKKQOTPAK 100

RESULT 5
MCPA_BOVIN STANDARD; PRT; 99 AA.
ID _MCPA_BOVIN
AC P28291;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Monocyte chemotactic protein 1A precursor (MCP-1A) (MCP-1) (Acidic
DE seminal fluid protein).
DE Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seminal plasma;
RX MEDLINE=92096117; PubMed=1721821;
RA Wempe F., Henschen A., Scheit K.H.;
RT "Gene expression and cDNA cloning identified a major basic protein
RT constituent of bovine seminal plasma as bovine
RT monocyte-chemoattractant protein-1 (MCP-1).";
RL DNA Cell Biol. 10:671-679(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Seminal plasma;
RX MEDLINE=92181448; PubMed=1543494;
RA Wempe F., Einspanier R., Scheit K.H.;
RT "Characterization by cDNA cloning of the mRNA of a new growth factor
RT from bovine seminal plasma: acidic seminal fluid protein.";
RL Biochem. Biophys. Res. Commun. 183:232-237(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=94338337; PubMed=8060303;
RA Wempe F., Kuhlmann J.K., Scheit K.H.;
RT "Characterization of the bovine monocyte chemoattractant protein-1
RT gene.";
RL Biochem. Biophys. Res. Commun. 202:1272-1279(1994).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC EMBL; L32659; AAA60956.1; -.
CC DR
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DR EMBL; M84602; AAA30651.1; -.
DR PIR; A39296; A39296.
DR HSP; P13500; 1DOM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein;
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 125 PYRROLIDONE CARBOXYLIC ACID (BY
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 125 AA; 13776 MW; 24C3A542CB6A47EE CRC64;
Query Match 77.5%; Score 314; DB 1; Length 125;
Best Local Similarity 75.0%; Pred. No. 8.6e-30;
Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
QY 1 QPDANAPVTCVYFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKICADPKQKWV 60
DB 24 QPDANVSPVTCVYFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKICADPKQKWV 83
QY 61 QDSMDHLDKQQTPTK 76
DB 84 QDAIANLDKMQTPTK 99
RESULT 7
MCPB_BOVIN STANDARD; PRT; 74 AA.
ID MCPB_BOVIN STANDARD; PRT; 74 AA.
AC P80343;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Monocyte chemotactic protein 1B (MCP-1B) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RC TISSUE=Kidney;
RX MEDLINE=95034774; PubMed=7947749;
RA Proost P., Wuyts A., Lenaerts J.-P., van Damme J.;
RT "Purification, sequence analysis, and biological characterization of
RT a second bovine monocyte chemotactic protein-1 (Bo MCP-1B).";
RL Biochemistry 33:13406-13412(1994).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils. Augments monocyte anti-tumor activity. Also induces
CC the release of Gelatinase B. This protein can bind heparin.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC HSP; P13500; 1DOK.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein;
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 125 PYRROLIDONE CARBOXYLIC ACID (BY
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 125 AA; 13776 MW; 24C3A542CB6A47EE CRC64;
Query Match 76.0%; Score 308; DB 1; Length 74;
Best Local Similarity 75.3%; Pred. No. 2.5e-29;
Matches 55; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 3 DAINAPVTCVYFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKICADPKQKWV 62
DB 1 DAINSPVTCVYFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKICADPKQKWV 60
```


DR EMBL; AF065936; AAF15386.1; -;
DR EMBL; AF065937; AAF15387.1; -;
DR EMBL; AF065938; AAF15388.1; -;
DR HSSP; PI3500; 1DOL.
DR MGD; MGI:108224; Ccl12.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response; Polymorphism.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 104 SMALL INDUCIBLE CYTOKINE A12.
FT DISULFID 33 58 BY SIMILARITY.
FT DISULFID 34 74 BY SIMILARITY.
FT VARIANT 94 104 QTFILPEPCLG -> RT (IN STRAIN SJL/J).
SQ SEQUENCE 104 AA; 11659 MW; 8D102F4FAC3DBF CRC64;

Query Match 70.1%; Score 284; DB 1; Length 104;
Best Local Similarity 68.1%; Pred. No. 2.3e-26;
Matches 49; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 2 PDAINAPVTCCYNFTNFKISVORLASRYRITSKPKKAVIPKTIKVAKEICADPKQKWVQ 61
DB 24 PDAVSTPVTCCYNVVKQKHVRKLKSYRITSQCPREAVIFRTILDKKEICADPKKWK 83

QY 62 DSWDHLDKOTOT 73
DB 84 NSINHLDKTSQT 95

RESULT 10
EOTA HUMAN STANDARD; PRT; 97 AA.
ID EOTA_HUMAN STANDARD; PRT; 97 AA.
AC P51671; P50877; Q92490; Q92491;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Botaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil
DE chemotactic protein).
GN CCL11 OR SCY11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96181758; PubMed=8597956;
RA Garcia-Zepeda E.A., Rothenberg M.E., Ownbey T.R., Leder P.,
RA Luster A.D.;
RT "Human eotaxin is a specific chemoattractant for eosinophil cells and
RT provides a new mechanism to explain tissue eosinophilia.";
RL Nat. Med. 2:449-456(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96189937; PubMed=8609214;
RA Ponath P.D., Qin S., Ringler D.J., Clark-Lewis I., Wang J., Kassam N.,
RA Smith H., Shi X., Gonzalo J.A., Newman W., Gutierrez-Ramos J.C.,
RA Mackay C.R.;
RT "Cloning of the human eosinophil chemoattractant, eotaxin. Expression,
RT receptor binding, and functional properties suggest a mechanism for
RT the selective recruitment of eosinophils.";
RL J. Clin. Invest. 97:604-612(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Small intestine;
RA Kitaura M., Nakajima T., Imai T., Harada S., Combadiere C.,
RA Tiffany H.L., Murphy P.M., Yoshie O.;
RT "Molecular cloning of human eotaxin, an eosinophil-selective CC
RT chemokine, and identification of a specific eosinophil eotaxin
RT receptor, CC chemokine receptor 3.";
RL J. Biol. Chem. 271:7725-7730(1996).

RESULT 9

SY12_MOUSE STANDARD; PRT; 104 AA.
AC Q62401; Q9QYD6;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Small inducible cytokine A12 precursor (CCL12) (Monocyte chemotactic
DE protein 5) (MCP-5) (MCP-1 related chemokine).
GN CCL12 OR SCYAL2 OR MCP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079149; PubMed=8920881;
RA Jia G.-Q., Gonzalo J.A., Lloyd C., Kremer L., Lu L., Martinez A.C.,
RA Wershil B.K., Gutierrez-Ramos J.C.;
RT "Distinct expression and function of the novel mouse chemokine
RT monocyte chemotactic protein-5 in lung allergic inflammation.";
RL J. Exp. Med. 184:1939-1951(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97149438; PubMed=8996246;
RA Sarafi M.N., Garcia-Zepeda E.A., McLean J.A., Charo I.F., Luster A.D.;
RT "Murine monocyte chemoattractant protein (MCP)-5: a novel CC
RT chemokine that is a structural and functional homologue of human
RT MCP-1.";
RL J. Exp. Med. 185:99-109(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=B10.S/J, BALB/c, DBA/2J, NOD/LTJ, and SJL/J; TISSUE=Spleen;
RX MEDLINE=99370037; PubMed=10498970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Scy1 (TCA-3), Scy2
RT (monocyte chemoattractant protein (MCP)-1), and Scy12 (MCP-5) are
RT candidates for eae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
CC -!- FUNCTION: Chemotactic factor that attracts eosinophils, monocytes,
CC and lymphocytes but not neutrophils. Potent monocyte active
CC chemokine that signals through CCR2. Involved in allergic
CC inflammation and the host response to pathogens and may play a
CC pivotal role during early stages of allergic lung inflammation.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- TISSUE SPECIFICITY: Predominantly expressed in the lymph nodes and
CC thymus. Also found in the salivary glands containing lymph nodes,
CC breast, heart, lung, brain, small intestine, kidney and colon.
CC -!- INDUCTION: By interferon gamma and lipopolysaccharides (LPS).
CC -!- POLYMORPHISM: The polymorphism in strain SJL/J may be associated
CC with severity of clinical symptoms of experimental allergic
CC encephalomyelitis, an animal model of multiple sclerosis, and
CC susceptibility to the monophasic remitting/nonrelapsing form of
CC the disease.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC EMBL; U50712; AAB50053.1; -;
DR EMBL; U66670; AAB49424.1; -;
DR EMBL; AF065934; AAF15384.1; -;
DR EMBL; AF065935; AAF15385.1; -;


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-----
CC      EMBL; X93886; CAA68168.1; ALT_INIT.
CC      EMBL; Y10802; CAA71760.1; -.
CC      EMBL; Y16645; CAA76341.1; -.
CC      PIR; JCS295; JC5295.
CC      PDB; 1ESR; 06-DEC-00.
CC      Genew; HGNC:10635; CCL8.
CC      MIM; 602283; -.
CC      GO; GO:0008009; F:Chemokine activity; TAS.
CC      GO; GO:0004871; F:Signal transducer activity; TAS.
CC      GO; GO:0006816; P:Calcium ion transport; TAS.
CC      GO; GO:0007267; P:Cell-cell signaling; TAS.
CC      GO; GO:0006935; P:Chemotaxis; TAS.
CC      GO; GO:0006887; P:exocytosis; TAS.
CC      GO; GO:0009615; P:response to viruses; TAS.
CC      GO; GO:0007165; P:signal transduction; TAS.
CC      InterPro; IPR000827; CC_Chemokine_sml.
CC      InterPro; IPR001811; Chemokine_IL8.
CC      Pfam; PF00048; IL8; 1.
CC      SMART; SM00199; SCV; 1.
CC      PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
CC      Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
CC      Polymorphism; Pyrrolidone carboxylic acid; 3D-structure.
CC      SIGNAL      1      23      PROBABLE.
CC      CHAIN      24      99      SMALL INDUCIBLE CYTOKINE A8.
CC      MOD RES      24      24      PYRROLIDONE CARBOXYLIC ACID.
CC      DISULFID      34      59      BY SIMILARITY.
CC      DISULFID      35      75      BY SIMILARITY.
CC      VARIANT      63      69      K -> Q.
CC      /FTID=VAR_001633.
CC      SEQUENCE 99 AA; 11246 MW; 9D67976BE9422F2A CRC64;
CC      FT FT
CC      SQ
Query Match .66.2%; Score 268; DB 1; Length 99;
Best Local Similarity 62.7%; Pred. No. 1.6e-24;
Matches 47; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
Qy 1 QPDAINAPVTCVCYFNFRKISVORLASYSRITSSKCPKEAVIFKTIYAKEICADPKQKW 60
Db 24 QPDSVSIPIPCFNVNINRKIPQIRLESYTRITNIQCPKEAVIFKTKRGEVCADPKRW 83
Qy 61 QDSMDHLDKQTQPK 75
Db 84 RDSKXHLDDQIFQNLK 98
RESULT 12
SY08_PIG
ID SY08_PIG STANDARD; PRT; 99 AA.
AC P49873;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
DE CCL8 OR SCYA8 OR MCP2.
OS Sus scrofa (Pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC [NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95091716; PubMed=7999015;
RA Hoang K.K., Knoke I.I., Klaudiny J.J., Wempe F.F., Wuttke W.W.,
RA Schell K.K.;
RT "Porcine luteal cells express monocyte chemoattractant protein-2

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RT (MCP-2): analysis by cDNA cloning and northern analysis."
 RL Biochem. Biophys. Res. Commun. 205:148-153(1994).
 CC -!- FUNCTION: Chemotactic factor that attracts monocytes. This protein
 CC can bind heparin.
 CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
 CC
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 CC
 CC -----
 DR EMBL; Z48480; CAA88371.1; -
 DR PIR; JC2417; JC2417.
 DR HSSP; P51671; 1E0T.
 DR InterPro: IPR000827; CC_chemokine_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 DR Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
 KW Pyrolidone carboxylic acid.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 39 SMALL INDUCIBLE CYTOKINE A8.
 FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY).
 FT DISULFID 34 59 BY SIMILARITY.
 FT DISULFID 35 75 BY SIMILARITY.
 SQ SEQUENCE 99 AA; 10903 MW; D3DAA0F7A964CDB1 CRC64;
 Query Match 64.4%; Score 261; DB 1; Length 99;
 Best Local Similarity 60.0%; Pred. No. 1.le-23;
 Matches 45; Conservative 16; Mismatches 14; Indels 0; Gaps 0;
 QY 1 OPDAINAPVTCYCNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETICADPKQKW 60
 Db 24 QPDSVSIITCCFGLVNGKIFPKKLESYTRITNSQCPQEAIVFKTKADKEVCADPQQKW 83
 QY 61 QSDMDHLKQQTTPK 75
 Db 84 QNSMKLLDQKSQTTPK 98
 RESULT 13
 SVL3_HUMAN
 ID SVL3_HUMAN STANDARD; PRT; 98 AA.
 AC Q99616; O95689;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Small inducible cytokine A13 precursor (CC13) (Monocyte chemotactic
 DE protein 4) (MCP-4) (Monocyte chemoattractant protein 4) (CX-beta-10)
 DE (NCC-1).
 DE GN CCL13 OR SCYA13 OR MCP4 OR NCC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RT TISSUE=Heart;
 RC MEDLINE=97113354; PubMed=8955214;
 RA Garcia-Zepeda E.A., Combadieere C., Rothenberg M.E., Sarafi M.N.,
 RA Lavigne P., Hamid O., Murphy P.M., Luster A.D.;
 RT "Human monocyte chemoattractant protein (MCP)-4 is a novel CC
 RT chemokine with activities on monocytes, eosinophils, and basophils
 RT induced in allergic and nonallergic inflammation that signals through
 RT the CC chemokine receptors (CCR)-2 and -3.";
 RL J. Immunol. 157:5613-5626(1996).
 RN [2]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-98.
 RT TISSUE=Fetal;
 RX MEDLINE=96235049; PubMed=8642349;
 RA Ugucioni M., Loetscher P., Forssmann U., Dewald B., Li H., Lima S.H.,
 RA Li Y., Kreider B., Garotta G., Thelen M., Baggiolini M.;
 RT "Monocyte chemotactic protein 4 (MCP-4), a novel structural and
 RT functional analogue of MCP-3 and ectaxin.";
 RL J. Exp. Med. 183:2379-2384(1996).
 RN [3]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-33.
 RT TISSUE=Fetal;
 RX MEDLINE=97341179; PubMed=915948;
 RA Berkhout T.A., Sarau H.M., Moores K., White J.R., Elshourbagy N.,
 RA Appelbaum E., Reape T.J., Branner M., Makwana J., Foley J.J.,
 RA Schmidt D.B., Imburgia C., Macnulty D., Matthews J., O'Donnell K.,
 RA O'Shannessy D., Scott M., Groot P.H.E., Macphee C.;
 RT "Cloning, in vitro expression, and functional characterization of a
 RT novel human CC chemokine of the monocyte chemotactic protein (MCP)
 RT family (MCP-4) that binds and signals through the CC chemokine
 RT receptor 2B.";
 RL J. Biol. Chem. 272:16404-16413(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RT Dante M., Gibson A.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RT TISSUE=Lung;
 RC Power C.A., Meyer A., Rison S.C.G., Guye-Coulin F., Wells T.N.C.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97213770; PubMed=9060459;
 RA Godiska R., Chantray D., Raport C.J., Schweickart V.L., Trong H.L.,
 RA Gray P.W.;
 RT "Monocyte chemotactic protein-4: tissue-specific expression and
 RT signaling through CC chemokine receptor-2.";
 RL J. Leukoc. Biol. 61:353-360(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RT TISSUE=Skin fibroblast;
 RX MEDLINE=99160888; PubMed=10049733;
 RA Hein H., Schluter C., Kulke R., Christophers E., Schroeder J.-M.,
 RA Bartels J.;
 RT "Genomic organization, sequence analysis and transcriptional
 RT regulation of the human MCP-4 chemokine gene (SCYA13) in dermal
 RT fibroblasts: a comparison to other eosinophilic beta-chemokines.";
 RL Biochem. Biophys. Res. Commun. 255:470-476(1999).
 RN [8]
 RP SEQUENCE FROM N.A.
 RT TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butler G.A., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]

RC TISSUE=Forebrain; 62.6%; Score 253.5; DB 1; Length 98;
RA Bartels J.H., Schlueter C., Richter E., Noso N., Christophers E.,
RA Schroeder J.-M.;
RT "Expression of a MCP-4 like novel CC-chemokine in human dermal
RL fibroblasts: molecular cloning and RT-PCR analysis."
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, lymphocytes,
CC basophils and eosinophils, but not neutrophils. Signals through
CC CCR2B and CCR3 receptors. Plays a role in the accumulation of
CC Leukocytes at both sides of allergic and nonallergic inflammation.
CC May be involved in the recruitment of monocytes into the arterial
CC wall during the disease process of arteriosclerosis. May play a
CC role in the monocyte attraction in tissues chronically exposed to
CC exogenous pathogens.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Widely expressed. Found in small intestine,
CC thymus, colon, lung, trachea, stomach and lymph node. Low levels
CC seen in the pulmonary artery smooth muscle cells.
CC -!- INDUCTION: By interleukin-1 and TNF-alpha.
CC -!- PFM: ONE MAJOR ISOFORM MCP-4, AND TWO MINOR ISOFORMS (LA) MCP-4 AND
CC (NPQGLA) MCP-4 ARE PRODUCED BY DIFFERENTIAL SIGNAL CLEAVAGE.
CC (LA) MCP-4 IS ABOUT 30 FOLD LESS ACTIVE THAN MCP-4.
CC -!- MASS SPECTROMETRY: MW=9314; NW ERR=30; METHOD=MALDI; RANGE=17-98.
CC -!- MASS SPECTROMETRY: MW=8760; NW ERR=30; METHOD=MALDI; RANGE=22-98.
CC -!- MASS SPECTROMETRY: MW=8575; NW ERR=30; METHOD=MALDI; RANGE=24-98.
CC -!- MISCELLANEOUS: This protein can bind heparin.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC -----
CC EMBL; U46767; AAB38703.1; -;
CC EMBL; AC002482; AAB67307.1; -;
CC EMBL; X98306; CAA66950.1; -;
CC EMBL; U59808; AAD09362.1; -;
CC EMBL; AJ001634; CAA04888.1; -;
CC EMBL; BC008621; AAB08621.1; -;
CC EMBL; Z77650; CAB01111.1; -;
CC HSSP; P51671; 1E0T.
CC Genew; HGNC:10611; CCL13.
CC MIM; 601391; -;
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0008009; F:chemokine activity; TAS.
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0006874; P:calcium ion homeostasis; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0006935; P:chemotaxis; TAS.
CC GO; GO:0006934; P:inflammatory response; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR000827; CC_chemokine_sml.
CC InterPro; IPR001811; Chemokine_I18.
CC InterPro; IPR008097; Fractalkine.
CC Pfam; PF00048; IL8; 1.
CC PRINTS; PR01721; FRCTALKINE.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Glycoprotein; Inflammatory response;
FT Pyrrolidone carboxylic acid.
FT SIGNAL
FT CHAIN
FT CHAIN 17 98 SMALL INDUCIBLE CYTOKINE A13, LONG FORM.
FT CHAIN 24 98 SMALL INDUCIBLE CYTOKINE A13, SHORT FORM.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 34 58 BY SIMILARITY.
FT DISULFID 35 74 BY SIMILARITY.
FT CARBOHYD 29 29 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 93 98 AHTLKT -> LTP (IN REF. 9).
SQ SEQUENCE 98 AA; 10986 MW; 612688DFCD308873 CRC64;

Query Match 62.6%; Score 253.5; DB 1; Length 98;
Best Local Similarity 60.5%; Pred. No. 7.8e-23;
Matches 46; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

QY 1 QPDANAPVTCYCNFTNRKISVQRLASRYRTSSKCPKEAVIFKTIYAKEICADPKQKW 60
Db 24 QPDALNPVSTCCTFSSKKISLQRLKSY-VITTSRCPQKAVIFRTKLGKEICADPKKW 82

QY 61 QBSMDHLDKQOTPKT 76
Db 83 QNYMKHLGRKAHTLKT 98

RESULT 14
SY02_MOUSE STANDARD; PRT; 148 AA.
ID SY02_MOUSE STANDARD; PRT; 148 AA.
AC P10148; Q9QVD7;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1) (Platelet-
DE derived growth factor-inducible protein JE).
DE CCL2 OR SCY2 OR MCP1 OR JE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093129; PubMed=2910858;
RA Kawahara R.S., Deuel T.F.;
RT "Platelet-derived growth factor-inducible gene JE is a member of a
RT family of small inducible genes related to platelet factor 4";
RL J. Biol. Chem. 264:679-682(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88234501; PubMed=3287374;
RA Rollins B.J., Morrison E.D., Stiles C.D.;
RT "Cloning and expression of JE, a gene inducible by platelet-derived
RT growth factor and whose product has cytokine-like properties";
RL Proc. Natl. Acad. Sci. U.S.A. 85:3738-3742(1988).
RN [3]
RP SEQUENCE FROM N.A.; AND VARIANTS GLY-50 AND GLN-92.
RC STRAIN=B10.S/J, BALB/c, DBA/2J, NOD/LTJ, and SJL/J; TISSUE=Spleen;
RX MEDLINE=99370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines SCY1 (TCA-3), SCY2
RT (monocyte chemoattractant protein (MCP)-1), and SCY12 (MCP-5) are
RT candidates for eae, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis";
RL J. Immunol. 163:2262-2266(1999).
RN [4]
RP SEQUENCE OF 26-42.
RX MEDLINE=91293127; PubMed=2065676;
RA van Damme J., Decock B., Bertini R., Conings R., Lenaerts J.-P.,
RA Put W., Opdenakker G., Mantovani A.;
RT "Production and identification of natural monocyte chemotactic
RT protein from virally infected murine fibroblasts. Relationship with
RT the product of the mouse competence (JE) gene";
RL Eur. J. Biochem. 199:223-229(1991).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By platelet-derived growth factor.
CC -!- POLYMORPHISM: The polymorphisms in strain SJL/J may be associated
CC with severity of clinical symptoms of experimental allergic
CC encephalomyelitis, an animal model of multiple sclerosis and
CC susceptibility to the monophasic remitting/nonrelapsing form of
CC the disease.

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OM protein - protein search, using sw model

Run on: August 30, 2004, 16:59:28 ; Search time 115 Seconds

(without alignments)
208.516 Million cell updates/sec

Title: 07330446.PEP

Perfect score: 405

Sequence: 1 qpdaipavtcycynftnrki.....qkwvqdsmdhldkgtqtpkt 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:**

- 1: sp_archaea:**
- 2: sp_bacteria:**
- 3: sp_fungi:**
- 4: sp_human:**
- 5: sp_invertebrate:**
- 6: sp_mammal:**
- 7: sp_mhc:**
- 8: sp_organelle:**
- 9: sp_phage:**
- 10: sp_plant:**
- 11: sp_rodent:**
- 12: sp_virus:**
- 13: sp_vertebrate:**
- 14: sp_unclassified:**
- 15: sp_rvirts:**
- 16: sp_bacteriap:**
- 17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 330 | 81.5 | 99 | 6 Q9TTQ3 | Q9ttq3 equus cabal |
| 2 | 297 | 73.3 | 109 | 6 Q865F3 | Q865f3 macaca mela |
| 3 | 287 | 70.9 | 109 | 4 Q727Q8 | Q727q8 homo sapien |
| 4 | 277 | 68.4 | 99 | 6 Q8MKC8 | Q8mkc8 equus cabal |
| 5 | 274 | 67.7 | 99 | 6 Q865F4 | Q865f4 macaca mela |
| 6 | 271 | 66.9 | 99 | 6 Q8HYQ0 | Q8hyq0 macaca mela |
| 7 | 261 | 64.4 | 97 | 6 Q8MI17 | Q8mit7 macaca mela |
| 8 | 261 | 64.4 | 97 | 6 Q8HXZ5 | Q8hxz5 macaca mela |
| 9 | 260 | 64.2 | 150 | 11 Q8CGM5 | Q8cgm5 sigmodon hi |
| 10 | 252 | 62.2 | 100 | 6 Q9TTQ4 | Q9ttq4 equus cabal |
| 11 | 249 | 61.5 | 97 | 11 Q9Z318 | Q9z318 cavia porce |
| 12 | 247 | 61.0 | 100 | 6 Q5MDP5 | Q5mdp5 bos taurus |
| 13 | 235 | 58.0 | 97 | 6 Q9TTQ6 | Q9ttq6 bos taurus |
| 14 | 211 | 52.1 | 81 | 6 Q9TTQ2 | Q9ttq2 equus cabal |
| 15 | 190.5 | 47.0 | 75 | 6 Q9TTQ1 | Q9ttq1 equus cabal |
| 16 | 183 | 45.2 | 62 | 4 Q95690 | Q95690 homo sapien |

| | | | | | |
|----|-------|------|-----|-----------|---------------------|
| 17 | 177 | 43.7 | 106 | 11 Q9Z292 | Q9z292 cricetus |
| 18 | 173 | 42.7 | 65 | 11 Q7TMS1 | Q7tms1 mus musculus |
| 19 | 156 | 38.5 | 44 | 6 Q9BG83 | Q9bg83 pongo pygma |
| 20 | 154 | 38.0 | 119 | 11 Q8K477 | Q8k477 rattus norv |
| 21 | 149.5 | 36.9 | 92 | 6 Q8MI76 | Q8mi76 bos taurus |
| 22 | 143.5 | 35.4 | 92 | 11 Q91ZL0 | Q91z10 sigmodon hi |
| 23 | 139.5 | 34.4 | 80 | 4 Q14745 | Q14745 homo sapien |
| 24 | 138.5 | 34.2 | 92 | 6 Q8HYQ2 | Q8hyq2 macaca mela |
| 25 | 137 | 33.8 | 91 | 13 Q8GG57 | Q8gg57 gallus gall |
| 26 | 136 | 33.6 | 89 | 11 Q8OX14 | Q8ox14 peromyscus |
| 27 | 135.5 | 33.5 | 56 | 6 Q8HYN4 | Q8hyn4 macaca mela |
| 28 | 135.5 | 33.5 | 90 | 13 Q9PWA6 | Q9pwa6 gallus gall |
| 29 | 134.5 | 33.2 | 91 | 13 Q8QG56 | Q8qg56 gallus gall |
| 30 | 134.5 | 33.2 | 92 | 4 Q8NHM4 | Q8nhw4 homo sapien |
| 31 | 133.5 | 33.0 | 93 | 6 Q8SOA6 | Q8sda6 bos taurus |
| 32 | 133.5 | 33.0 | 93 | 11 Q9ERE0 | Q9ere0 rattus norv |
| 33 | 132.5 | 32.7 | 92 | 6 Q8HYQ3 | Q8hyq3 macaca mela |
| 34 | 130 | 32.1 | 131 | 6 Q8HYP5 | Q8hyp5 macaca mela |
| 35 | 128.5 | 31.7 | 91 | 13 Q8JIMS | Q8jms paralichthy |
| 36 | 128.5 | 31.7 | 91 | 13 Q8AV56 | Q8av56 paralichthy |
| 37 | 128.5 | 31.7 | 101 | 12 Q8TR57 | Q8trs7 guinea pig |
| 38 | 128 | 31.6 | 395 | 11 Q8C9Y1 | Q8c9y1 mus musculus |
| 39 | 128 | 31.6 | 395 | 11 Q9IV44 | Q9iv44 mus musculus |
| 40 | 127.5 | 31.5 | 91 | 13 Q8JIM4 | Q8jim4 paralichthy |
| 41 | 126.5 | 31.2 | 85 | 11 Q80XG5 | Q8oxg5 peromyscus |
| 42 | 124.5 | 30.7 | 99 | 6 Q95N01 | Q95n01 canis fami |
| 43 | 120.5 | 29.8 | 97 | 13 Q57411 | Q57411 gallus gall |
| 44 | 119 | 29.4 | 407 | 6 Q865F6 | Q865f6 macaca mela |
| 45 | 119 | 29.4 | 408 | 6 Q8HXZ1 | Q8hxz1 macaca mela |

ALIGNMENTS

RESULT 1

| | | | |
|--------|---|--------|-----------------------------------|
| Q9TTQ3 | PRELIMINARY; | PRT; | 99 AA. |
| ID | Q9TTQ3 | | |
| AC | Q9TTQ3; | | |
| DT | 01-MAY-2000 (TrEMBLrel. 13, Created) | | |
| DT | 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) | | |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) | | |
| DE | Monocyte chemoattractant protein-1 precursor. | | |
| GN | MCP-1. | | |
| OS | Equus caballus (Horse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Perissodactyla; Equidae; Equus. | | |
| OX | NCBI_TaxID=9796; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=Lung; | | |
| RX | MEDLINE=21061912; PubMed=11044560; | | |
| RA | Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W., | | |
| RA | Collins M.E.; | | |
| RT | "Cloning of equine chemokines eotaxin, monocyte chemoattractant | | |
| RT | protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and | | |
| RT | induction by IL-4 in dermal fibroblasts."; | | |
| RL | Vet. Immunol. Immunopathol. 76:293-298(2000). | | |
| DR | EMBL; AJ251189; CAB61625.1; - | | |
| DR | HSSP; P13500; 1DOM. | | |
| DR | GO; GO:0005576; C:extracellular; IEA. | | |
| DR | GO; GO:0008009; F:chemokine activity; IEA. | | |
| DR | GO; GO:0006955; P:immune response; IEA. | | |
| DR | InterPro; IPR000827; CC_chemokine_sml. | | |
| DR | InterPro; IPR001811; Chemokine_IL8. | | |
| DR | PFAM; PF00048; IL8; 1. | | |
| DR | SMART; SM00199; SCY; 1. | | |
| DR | PROSITE; PS00472; SMALL_CYTOKINES_CC; 1. | | |
| KW | SIGNAL. | 1 | 23 |
| FT | POTENTIAL. | | |
| FT | CHAIN | 24 | 99 |
| SQ | SEQUENCE | 99 AA; | 10790 MW; BA1448F79F3423D2 CRC64; |

Query Match 81.5%; Score 330; DB 6; Length 99;

Best Local Similarity 78.7%; Pred. No. 2.5e-33; Mismatches 9; Conservative 9; Indels 0; Gaps 0;
 RT assignment to the C-C chemokine gene cluster on chromosome 17q11.2-
 RT q12.2;
 RL Genomics 21:403-408(1994).
 DR EMBL: X72309; CABS9723.1; -.
 SQ SEQUENCE 109 AA; 12356 MW; 69380669FOA2157D CRC64;
 Query Match 70.9%; Score 287; DB 4; Length 109;
 Best Local Similarity 72.0%; Pred. No. 6.4e-28;
 Matches 54; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
 QY 1 QPDAINAPVTCYNTNFKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 24 QPDAINSPTCCYPTGKISSQRLGSKYKVTSSKCPKEAVIFKTIIVAKEICADPEQKW 83
 QY 61 QDSMDHLDKQTQTPK 75
 DB 84 QDAVKQLDKKAQTPK 98

RESULT 2
 ID Q865F3 PRELIMINARY; PRT; 109 AA.
 AC Q865F3;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Monocyte chemoattractant protein-3.
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Coleman G.D., Valli P.J.S., Clements J.E., Zink M.C.;
 RT "Macaca nemestrina (Pig-tailed macaque) monocyte chemoattractant
 protein-3 (MCP-3).";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY206694; AA052735.1; -.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0008009; F:chemokine activity; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR000827; CC:chemokine_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 SQ SEQUENCE 109 AA; 12346 MW; D031826233EC461A CRC64;
 Query Match 73.3%; Score 297; DB 6; Length 109;
 Best Local Similarity 73.3%; Pred. No. 3.6e-29;
 Matches 55; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
 QY 1 QPDAINAPVTCYNTNFKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 34 QPDGINTSTTCYRINKIPKQRLSYRRITSSKCPKEAVIFKTIIVAKEICADPTQKW 93
 QY 61 QDSMDHLDKQTQTPK 75
 DB 94 QBFMKHLDDKQTQTPK 108

RESULT 3
 ID Q727Q8 PRELIMINARY; PRT; 109 AA.
 AC Q727Q8;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Monocyte chemoattractant protein-3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94375065; PubMed=7916328;
 RA Opdenakker G.M.M.;
 RT "The human MCP-3 gene (SCYA7): cloning, sequence analysis, and

RT assignment to the C-C chemokine gene cluster on chromosome 17q11.2-
 RT q12.2;
 RL Genomics 21:403-408(1994).
 DR EMBL: X72309; CABS9723.1; -.
 SQ SEQUENCE 109 AA; 12356 MW; 69380669FOA2157D CRC64;
 Query Match 70.9%; Score 287; DB 4; Length 109;
 Best Local Similarity 72.0%; Pred. No. 6.4e-28;
 Matches 54; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
 QY 1 QPDAINAPVTCYNTNFKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 34 QPDGINTSTTCYRINKIPKQRLSYRRITSSKCPKEAVIFKTIIVAKEICADPTQKW 93
 QY 61 QDSMDHLDKQTQTPK 75
 DB 94 QBFMKHLDDKQTQTPK 108

RESULT 4
 ID Q8MKC8 PRELIMINARY; PRT; 99 AA.
 AC Q8MKC8;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE MCP-2.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
 RT "Equus caballus monocyte chemoattractant protein-2 (mcp-2), complete
 cds";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF506972; AA034214.1; -.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0008009; F:chemokine activity; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 SQ SEQUENCE 99 AA; 11028 MW; 94F5D8E540889228 CRC64;
 Query Match 68.4%; Score 277; DB 6; Length 99;
 Best Local Similarity 65.3%; Pred. No. 1e-26;
 Matches 49; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
 QY 1 QPDAINAPVTCYNTNFKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 24 QPDAINSPTCCYRINKIPKQRLSYRRITSSKCPKEAVIFKTIIVAKEICADPTQKW 83
 QY 61 QDSMDHLDKQTQTPK 75
 DB 84 QDFMKHLDDKQTQTPK 98

RESULT 5
 ID Q865F4 PRELIMINARY; PRT; 99 AA.
 AC Q865F4;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Monocyte chemoattractant protein-2.
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9545;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Coleman G.D., Clements J.E., Zink M.C.; MCP-2 (CC) chemokine."
 RT "Macaca nemestrina (pig-tailed macaque) MCP-2 (CC) chemokine."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY206693; AAC52734.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008009; P:immune response; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000827; CC:chemokine_sml.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR InterPro; IPR008097; Fractalkine.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR01721; FRCTALKINE.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 SQ SEQUENCE 99 AA; 11263 MW; 9D6797974A88BF7F CRC64;

Query Match 67.7%; Score 274; DB 6; Length 99;
 Best Local Similarity 62.7%; Pred. No. 2.4e-26;
 Matches 47; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 OPDANAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKICADPKKWV 60
 DB 24 QPDSVSIPTCCFNVINRKIPQRLQSYTRITNQCPKEAVIFKTKWKEVCADPKERW 83
 QY 61 QDSMDHLDKQTQTPK 75
 DB 84 RDSMKHLDQIFQNLK 98

RESULT 6

Q8HYQ0 PRELIMINARY; PRT; 99 AA.
 AC Q8HYQ0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Chemokine CC18/MCP-2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

SEQUENCE FROM N.A.

RP Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
 RA "Comprehensive cloning and sequencing reveals evolutionary
 RT conservation among all groups of rhesus macaque chemokines."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF449289; AAN76073.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008009; P:immune response; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000827; CC:chemokine_sml.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR InterPro; IPR008097; Fractalkine.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR01721; FRCTALKINE.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 SQ SEQUENCE 99 AA; 11263 MW; 9D6797974A88BF7F CRC64;

Query Match 66.9%; Score 271; DB 6; Length 99;
 Best Local Similarity 62.7%; Pred. No. 5.7e-26;
 Matches 47; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 OPDANAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKICADPKKWV 60
 DB 24 QPDSVSIPTCCFNVINRKIPQRLQSYTRITNQCPKEAVIFKTKWKEVCADPKERW 83
 QY 61 QDSMDHLDKQTQTPK 75

DB 84 RDSMKHLDQIFQNLK 98

RESULT 7

Q8MIT7 PRELIMINARY; PRT; 97 AA.
 ID Q8MIT7;
 AC Q8MIT7;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Eotaxin.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

SEQUENCE FROM N.A.

RP Zhang L., Soares M.P., Guan Y., Sirotina-Weisher A.,
 RA Matheravadahu S., Iliff S.A., Mudgett J.S., Springer M.S.,
 RA Daugherty B.L.;

RT "Molecular cloning of eotaxin/CCL11 and CCR3 from rhesus monkey.
 RT Functional expression and characterization of rhesus monkey CCR3 in
 RT murine Li-2 cells; generation of antibodies against rhesus CCR3."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY049019; AAL13086.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008009; F:chemokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000827; CC:chemokine_sml.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 SQ SEQUENCE 97 AA; 10855 MW; 9BCA0FD6D95B02DD CRC64;

Query Match 64.4%; Score 261; DB 6; Length 97;
 Best Local Similarity 63.5%; Pred. No. 9.8e-25;
 Matches 47; Conservative 14; Mismatches 11; Indels 2; Gaps 1;

QY 2 PDANAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKICADPKKWV 61
 DB 25 PDSV--ATTCCFTLNKKIPQRLQSYTRITNQCPKEAVIFKTKWKEVCADPKKWV 82
 QY 62 DSMHLDKQTQTPK 75
 DB 83 DSMKYLDRKSPFK 96

RESULT 8

Q8HXZ5 PRELIMINARY; PRT; 97 AA.
 ID Q8HXZ5;
 AC Q8HXZ5;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Chemokine CCL11/eotaxin.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

SEQUENCE FROM N.A.

RP Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
 RA "Comprehensive cloning and sequencing reveals evolutionary
 RT conservation among all groups of rhesus macaque chemokines."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF449270; AAN76074.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008009; F:chemokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 97 AA; 10795 MW; ED0CD432880A47C9 CRC64;

Query Match 64.4%; Score 261; DB 6; Length 97;
Best Local Similarity 63.5%; Pred. No. 9.8e-25;
Matches 47; Conservative 14; Mismatches 11; Indels 2; Gaps 1;

QY 2 PDANAPVTCYVFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 61
Db PDSV--ATTCFTLTNKILPQLRLESYRRIISGKCPQKAVIFKTKLAKDICADPKQKWV 82

QY 62 DSMHLDKQOTPK 75
Db DSMKYLDKSPK 96

RESULT 9
Q8CGM5 PRELIMINARY; PRT; 150 AA.
AC Q8CGM5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monocyte chemoattractant protein-1.
GN MCP-1/UE.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
SEQUENCE FROM N.A.
RA Blanco J.C.; Pletneva L.M.; Prince G.A.;
RP "Sigmodon hispidus cytokines, chemokines and interferons.";
RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY165953; AAN85636.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0008955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 150 AA; 16480 MW; 16341DBD2C52AF25 CRC64;

Query Match 64.2%; Score 260; DB 11; Length 150;
Best Local Similarity 63.2%; Pred. No. 2.1e-24;
Matches 48; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 QPDANAPVTCYVFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db QPDANAPVTCYVFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 84

QY 61 QDSMDHLDKQOTPK 76
Db QMYTKMDQNKARSET 100

RESULT 10
Q9TTQ4 PRELIMINARY; PRT; 100 AA.
AC Q9TTQ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Eotaxin precursor.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21061912; PubMed=11044560;
RA Benarafa C.; Cunningham F.M.; Hamblin A.S.; Horohov D.W.;
RA Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and induction by IL-4 in dermal fibroblasts";
RT Vet. Immunol. Immunopathol. 76:283-298(2000).
RL EMBL; AJ251188; CAB61624.1; -
DR HSP; P51671; IEOT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0008955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 100 EOTAXIN.
SQ SEQUENCE 100 AA; 11247 MW; 11F08EC00E75D50B CRC64;

Query Match 62.2%; Score 252; DB 6; Length 100;
Best Local Similarity 64.0%; Pred. No. 1.3e-23;
Matches 48; Conservative 13; Mismatches 12; Indels 2; Gaps 1;

QY 1 QPDANAPVTCYVFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db QPVSSIS--TVCCFNVASRKISFQRLQSYRKITSSKCPQKAVIFKTKQAKKICADPKQKWV 81

QY 61 QDSMDHLDKQOTPK 75
Db QDAMKYLDENSRITK 96

RESULT 11
Q9Z318 PRELIMINARY; PRT; 97 AA.
ID Q9Z318
AC Q9Z318; (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Monocyte chemoattractant protein-3 (MCP-3).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Lung;
RP Asano K.; Nakamura M.; Oguma T.; Fukunaga K.; Matsubara H.;
RA Ishizaka A.; Yamaguchi K.; Kanazawa M.;
RT "Differential expression of CC chemokines in guinea pig lungs during an allergic inflammation";
RT Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB014340; BAA36456.1; -
DR HSP; P51671; IEOT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0008955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 97 AA; 11155 MW; E1B9A17C165C2421 CRC64;

RA Query Match 61.5%; Score 249; DB 11; Length 97;
RT Best Local Similarity 63.2%; Pred. No. 3.1e-23;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF399641; AAK94451.1; -
DR HSSP; Q9Y258; IG28.
QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDGWNIS-TCCKY-RSQIRVORLESVTRITSSKCPQWAVIFKTKENREICADPKQWV 81
QY 61 QDSMDHLDKQTQPKT 76
Db 82 QDSMKYIDKSKTPKS 97

RESULT 12
Q95MDS PRELIMINARY; PRT; 100 AA.
AC Q95MDS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemoattractant protein 2 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Weeling D.;
RT "Role of chemokines in respiratory syncytial virus infection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF399641; AAK94451.1; -
DR HSSP; Q9Y258; IG28.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SWALL_CYTOKINES_CC; 1.
FT NON TER 1
SQ SEQUENCE 100 AA; 11001 MW; FID308AD924FCAP6 CRC64;

Query Match 61.0%; Score 247; DB 6; Length 100;
Best Local Similarity 56.0%; Pred. No. 5.6e-23;
Matches 42; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 25 QPDSVSTITCCFVINGKIFKLLDSYTRITNSQCPQEAIVFKTKADRDVCAADPKQKW 84
QY 61 QDSMDHLDKQTQPK 75
Db 85 QTSIRLLDQKSTPK 99

RESULT 13
Q9TTS6 PRELIMINARY; PRT; 97 AA.
AC Q9TTS6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Eotaxin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

RA Query Match 58.0%; Score 235; DB 6; Length 97;
RT Best Local Similarity 55.3%; Pred. No. 1.7e-21;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132003; CAB61617.1; -
DR HSSP; P51671; IEOT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR SEQUENCE 97 AA; 10965 MW; 9E65F23E1DDEB743 CRC64;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPASI--PTICFNMSKKKISIQRLQSYRKRISSKCPQWAVIFKTKQNKKKI CVDPKQWV 81
QY 61 QDSMDHLDKQTQPKT 76
Db 82 QNAMEYLNQSKQTLS 97

RESULT 14
Q9TTQ2 PRELIMINARY; PRT; 81 AA.
AC Q9TTQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Monocyte chemoattractant protein-2 precursor (Fragment).
GN MCP-2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21061912; PubMed=11045560;
RA Benarafa C.; Cunningham F.M.; Hamblin A.S.; Horohov D.W.;
RA Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and RT induction by IL-4 in dermal fibroblasts."
RL Vet. Immunol. Immunopathol. 76:283-298 (2000).
DR EMBL; AJ251190; CAB61626.1; -
DR HSSP; P13500; IDOK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL
FT CHAIN 24 >81 BY SIMILARITY.
FT NON TER 81
SQ SEQUENCE 81 AA; 8858 MW; A34ADE103C386B0F CRC64;

Query Match 52.1%; Score 211; DB 6; Length 81;
Best Local Similarity 65.5%; Pred. No. 1.4e-18;
Matches 38; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQK 58
Db 24 QPDASVPTVTCFVINGKVPFQRLQSYRKRISSKCPQWAVIFKTKVDEICADPKKK 81

RESULT 15

Q9TTQ1
ID Q9TTQ1 PRELIMINARY; PRT; 75 AA.
AC Q9TTQ1;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Monocyte chemoattractant protein-4 precursor (Fragment).
GN MCP-4.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]_TaxID=9796;
RP SEQUENCE FROM N.A.
RX MEDLINE=21061912; PubMed=11044560;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
RA Collins M.E.;
RT "Cloning of equine chemokines sotaxin, monocyte chemoattractant
protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
induction by IL-4 in dermal fibroblasts";
RL Vet. Immunol. Immunopathol. 76:283-298(2000).
DR EMBL; AJ251191; CAB61627.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR HSP; P51671; LEOT.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW Signal.
FT NON TER 1 1
FT SIGNAL <1 18 POTENTIAL.
FT CHAIN 19 >75 MONOCYTE CHEMOATTRACTANT PROTEIN-4.
FT NON TER 75 75
SQ SEQUENCE 75 AA; 8277 MW; 480A5267AC6A03E5 CRC64;
Query Match 47.0%; Score 190.5; DB 6; Length 75;
Best Local Similarity 58.6%; Pred. No. 4.5e-16;
Matches 34; Conservative 14; Mismatches 9; Indels 1; Gaps 1;
QY 1 OPDAINPVTCYFTNEKISVORLASVERITSSKCPKEAVIFKTIYAKEICADPKOK 58
Db 19 QFDALSAUTACCFNFKMPLQLRYSY-RITGSCPOEAVIFRTKLAKDVCAADPKKK 75

Search completed: August 30, 2004, 17:07:19
Job time : 119 secs

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:49:12 ; Search time 1389 Seconds
(without alignments)
7114.623 Million cell updates/sec

Title: 07330446
Perfect score: 228
Sequence: 1 cagccgatgcaatcaatgc.....aaacccaaactccgaagact 228

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
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- 15: em.ba.*
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- 32: em.htg_other.*
- 33: em.htg_mus.*
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- 35: em.htg_rod.*
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- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match % | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|-------------|
| 1 | 228 | 100.0 | 228 | 6 | BD102671 |
| 2 | 228 | 100.0 | 228 | 6 | BD137507 |
| 3 | 228 | 100.0 | 300 | 6 | BD168034 |
| 4 | 228 | 100.0 | 300 | 6 | BD177097 |
| 5 | 228 | 100.0 | 300 | 12 | BT007880 |
| 6 | 228 | 100.0 | 418 | 6 | E05615 |
| 7 | 228 | 100.0 | 554 | 6 | E05599 |
| 8 | 228 | 100.0 | 647 | 6 | AX698741 |
| 9 | 228 | 100.0 | 725 | 6 | AR337874 |
| 10 | 228 | 100.0 | 725 | 6 | AR380799 |
| 11 | 228 | 100.0 | 725 | 6 | AX774742 |
| 12 | 228 | 100.0 | 725 | 9 | HSNCP1 |
| 13 | 228 | 100.0 | 739 | 6 | AX577974 |
| 14 | 228 | 100.0 | 739 | 9 | S71513 |
| 15 | 228 | 100.0 | 741 | 6 | A17786 |
| 16 | 228 | 100.0 | 741 | 6 | AR094465 |
| 17 | 228 | 100.0 | 741 | 6 | E05611 |
| 18 | 228 | 100.0 | 741 | 6 | AR380620 |
| 19 | 228 | 100.0 | 741 | 9 | HUNMCAF |
| 20 | 228 | 100.0 | 743 | 9 | BC009716 |
| 21 | 228 | 100.0 | 978 | 6 | AX838969 |
| 22 | 228 | 100.0 | 978 | 6 | BD222013 |
| 23 | 228 | 100.0 | 984 | 6 | AX838970 |
| 24 | 228 | 100.0 | 984 | 6 | BD222014 |
| 25 | 228 | 100.0 | 999 | 6 | AX838971 |
| 26 | 228 | 100.0 | 999 | 6 | BD222015 |
| 27 | 227.6 | 99.8 | 1712 | 6 | AR352699 |
| 28 | 227.6 | 99.8 | 1712 | 6 | BD195644 |
| 29 | 227.6 | 99.8 | 1822 | 6 | AR352698 |
| 30 | 227.6 | 99.8 | 1822 | 6 | BD195643 |
| 31 | 227.2 | 99.6 | 330 | 6 | E03542 |
| 32 | 227.2 | 99.6 | 330 | 6 | E03044 |
| 33 | 226.4 | 99.3 | 300 | 9 | BT007329 |
| 34 | 226.4 | 99.3 | 356 | 6 | BD058323 |
| 35 | 226.4 | 99.3 | 382 | 6 | BD058320 |
| 36 | 226.4 | 99.3 | 661 | 6 | BD080551 |
| 37 | 226.4 | 99.3 | 661 | 9 | S69738 |
| 38 | 226.4 | 99.3 | 718 | 9 | HUMSECPA |
| 39 | 224.8 | 98.6 | 228 | 6 | I28478 |
| 40 | 218.4 | 95.8 | 300 | 9 | AF255343 |
| 41 | 218.4 | 95.8 | 300 | 9 | AF449265 |
| 42 | 216.8 | 95.1 | 300 | 9 | AF276081 |
| 43 | 216.8 | 95.1 | 300 | 9 | AY206692 |
| 44 | 211.2 | 92.6 | 361 | 6 | BD058318 |
| 45 | 205.2 | 90.0 | 279 | 6 | BD168033 |

ALIGNMENTS

RESULT 1
BD102671
LOCUS
DEFINITION Composition for treating or preventing primary pulmonary hypertension.
ACCESSION BD102671
VERSION BD102671.1 GI:22648245
KEYWORDS WO 0189582-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 228)
AUTHORS Bgashira,K., Yonemitsu,Y., Sueishi,K., Ikeda,Y. and Inada,Y.
TITLE Composition for treating or preventing primary pulmonary

BD102671 228 bp DNA linear PAT 27-AUG-2002
Composition for treating or preventing primary pulmonary

JOURNAL Patent: WO 0189582-A 1 29-NOV-2001;
TAKEDA CHEMICAL INDUSTRIES LTD KENSUKE EGASHIRA, YOSHIKAZU
YONEMITSU, KATSUO SUEISHI, YASUHIRO IKEDA, YOSHIYUKI INADA
COMMENT OS Homo sapiens (human)
PN WO 0189582-A/1
PD 29-NOV-2001
PF 25-MAY-2001 WO 2001JP004381
PR 26-MAY-2000 JP OOP 161145
PI KENSUKE EGASHIRA, YOSHIKAZU YONEMITSU, KATSUO SUEISHI, YASUHIRO
IKEDA,
PI YOSHIYUKI INADA
PC A61K48/00, A61K39/395, A61K31/711, A61P11/00, A61P9/12
CC Composition for treating or preventing primary pulmonary CC
hypertension
FH Key Location/Qualifiers
FT source 1..228 /organism='Homo sapiens (human)'.
FT Location/Qualifiers
1..228
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

FEATURES source
Query Match 100.0%; Score 228; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 7.2e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
1 CAGCCAGATGCAATCAATGCCCGACCTGCTGTATTAACCTCACCATAAGGAGATC 60
1 CAGCCAGATGCAATCAATGCCCGACCTGCTGTATTAACCTCACCATAAGGAGATC 60
61 TCAGTCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
61 TCAGTCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
121 GTGATCTTCAGACCAATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
121 GTGATCTTCAGACCAATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228
181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228

RESULT 3
BD168034 300 bp DNA linear PAT 17-JAN-2003
LOCUS Novel hepatic disease agent.
DEFINITION
ACCESSION BD168034
VERSION BD168034.1 GI:27873846
KEYWORDS WO 0230464-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 300)
AUTHORS Egashira, K., Takeshita, A., Koyanagi, M., Nakamura, M. and Nishida, K.
TITLE Novel hepatic disease agent
JOURNAL Patent: WO 0230464-A 2 18-APR-2002;
KENSUKE EGASHIRA, DAIICHI PHARMACEUTICAL CO LTD, AKIRA TAKESHITA,
NASAMICHI KOYANAGI, MAKOTO NAKAMURA, KENICHI NISHIDA
COMMENT OS Homo sapiens (human)
PN WO 0230464-A/2
PD 18-APR-2002
PF 28-SEP-2001 WO 2001JP008552
PR 11-OCT-2000 JP OOP 310604
PI KENSUKE EGASHIRA, AKIRA TAKESHITA, MASAMICHI KOYANAGI, MAKOTO PI
NAKAMURA,
PI KENICHI NISHIDA
PC A61K45/00, A61K48/00, A61P43/00, A61P1/16
CC Novel hepatic disease agent
FH Key Location/Qualifiers
FT source 1..300 /organism='Homo sapiens (human)'.
FT Location/Qualifiers
1..300
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

FEATURES source
Query Match 100.0%; Score 228; DB 6; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
1 CAGCCAGATGCAATCAATGCCCGACCTGCTGTATTAACCTCACCATAAGGAGATC 60
1 CAGCCAGATGCAATCAATGCCCGACCTGCTGTATTAACCTCACCATAAGGAGATC 60
61 TCAGTCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
61 TCAGTCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
121 GTGATCTTCAGACCAATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
121 GTGATCTTCAGACCAATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228
181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228

RESULT 2
BD137507 228 bp DNA linear PAT 18-SEP-2002
LOCUS Preventive or remedy for pulmonary hypertension.
DEFINITION
ACCESSION BD137507
VERSION BD137507.1 GI:23232452
KEYWORDS JP 2002047203-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 228)
AUTHORS Egashira, K., Yonemitsu, Y., Sueishi, K., Ikeda, Y. and Inada, Y.
TITLE Preventive or remedy for pulmonary hypertension
JOURNAL Patent: JP 2002047203-A 1 12-FEB-2002;
KENSUKE EGASHIRA, TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 2002047203-A/1
PD 12-FEB-2002
PF 25-MAY-2001 JP 2001156252
PR KENSUKE EGASHIRA, YOSHIKAZU YONEMITSU, KATSUO SUEISHI, YASUHIRO
IKEDA,
PI YOSHIYUKI INADA
PC A61K38/00, A61K31/7088, A61K39/395, A61K39/395, A61K48/00, A61P9/12,
PC A61P11/00, C07K14/52, C07K16/24//C12N15/09, A61K37/02, C12N15/00
CC Preventive or remedy for pulmonary hypertension FH Key
Location/Qualifiers

Db 70 CAGCAGATGCAATCAATGCCAGTCCACCTGCTGTATTAACTTACCAATAGGAAGATC 129
Qy 61 TCAGTGCAGAGGCTCGGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT 120
Db 130 TCAGTGCAGAGGCTCGGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT 189
Qy 121 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTCTGACCCCAAGCAGAGAGTGGTT 180
Db 190 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTCTGACCCCAAGCAGAGAGTGGTT 249
Qy 181 CAGGATTCATGGACCACTGGACCAAGCAACCAAACTCCGAAGACT 228
Db 250 CAGGATTCATGGACCACTGGACCAAGCAACCAAACTCCGAAGACT 297

RESULT 4
BD177097 300 bp DNA linear PAT 16-APR-2003
LOCUS
DEFINITION Prophylactic and/or remedy for vascular restenosis.
BD177097
ACCESSION BD177097.1 GI:30014357
VERSION JP 2002284698-A/2.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 300)
REFERENCE
AUTHORS Egashira,K. and Takeshita,A.
TITLE Prophylactic and/or remedy for vascular restenosis
JOURNAL Patent: JP 2002284698-A 2 03-OCT-2002;
KENSUKE EGASHIRA, DAIICHI PHARMACEUTICAL CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2002284698-A/2
PD 03-OCT-2002
PF 23-MAR-2001 JP 2001085073
PI KENSUKE EGASHIRA, AKIRA TAKESHITA
PC
A61K45/00, A61K31/711, A61K35/76, A61K38/00, A61K39/395, A61K39/395, PC
A61K48/00,
PC A61P9/10, A61P9/10//C12N15/09, A61K37/02, C12N15/00 CC
Prophylactic and/or remedy for vascular restenosis FH Key
Location/Qualifiers
FT source 1..300
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..300
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
ORIGIN
Query Match 100.0%; Score 228; DB 6; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e-57; Mismatches 0; Indels 0; Gaps 0;
Matches 228; Conservative 0;
Qy 1 CAGCAGATGCAATCAATGCCAGTCCACCTGCTGTATTAACTTACCAATAGGAAGATC 60
Db 70 CAGCAGATGCAATCAATGCCAGTCCACCTGCTGTATTAACTTACCAATAGGAAGATC 129
Qy 61 TCAGTGCAGAGGCTCGGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT 120
Db 130 TCAGTGCAGAGGCTCGGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT 189
Qy 121 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTCTGACCCCAAGCAGAGAGTGGTT 180
Db 190 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTCTGACCCCAAGCAGAGAGTGGTT 249
Qy 181 CAGGATTCATGGACCACTGGACCAAGCAACCAAACTCCGAAGACT 228
Db 250 CAGGATTCATGGACCACTGGACCAAGCAACCAAACTCCGAAGACT 297

RESULT 5

BT007880 300 bp mRNA linear SYN 13-MAY-2003
LOCUS
DEFINITION Synthetic construct Homo sapiens chemokine (C-C motif) ligand 2
BT007880
ACCESSION BT007880.1 GI:30584598
VERSION FL1_CDNA.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Kaline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 300)
AUTHORS Kaline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA
COMMENT This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
FEATURES
Location/Qualifiers
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/organism='synthetic construct'
/mol_type='mRNA'
/db_xref='taxon:32630'
/clone='GH00237L1.0'
/clone_lib='BD Creator(TM) CDS Library derived from MGC
collection'
/lab_host='DH5alpha Tl resistant'
/notes='Vector: pDNR-Dual'
1..>300
/notes='Mutations: 299:Stop->Leu'
/codon_start=1
/transl_table=11
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/protein_id='AAB3652.1'
/db_xref='GI:30584599'
/translation='MKVSAALLCLLIATFIPOGLAQPDAINAPVTCVNFNPKIL
VQSLASVRITSSKPKKAVIFKTIIVAKEICADPKQKQVQDSMDHLDKQTPTKTL'
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Best Local Similarity 100.0%; Pred. No. 7.3e-57; Mismatches 0; Indels 0; Gaps 0;
Matches 228; Conservative 0;
Qy 1 CAGCAGATGCAATCAATGCCAGTCCACCTGCTGTATTAACTTACCAATAGGAAGATC 60
Db 70 CAGCAGATGCAATCAATGCCAGTCCACCTGCTGTATTAACTTACCAATAGGAAGATC 129
Qy 61 TCAGTGCAGAGGCTCGGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT 120
Db 130 TCAGTGCAGAGGCTCGGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT 189
Qy 121 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTCTGACCCCAAGCAGAGAGTGGTT 180
Db 190 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTCTGACCCCAAGCAGAGAGTGGTT 249
Qy 181 CAGGATTCATGGACCACTGGACCAAGCAACCAAACTCCGAAGACT 228

Db 250 CAGGATTCATGGACCACTGGACAGCAAGCAACCACTCGAAGACT 297

RESULT 6
 LOCUS E05615
 DEFINITION Synthetic DNA.
 ACCESSION E05615
 VERSION E05615.1 GI:2173802
 KEYWORDS JP 1993260987-A/19
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE
 1 (bases 1 to 418)
 Yamagishi,J., Matsuo,T., Fukui,J. and Yamada,M.
 PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYPEPTIDE AND MICROBIAL STRAIN PRODUCING THE POLYPEPTIDE
 Patent: JP 1993260987-A 19 12-OCT-1993;
 DAINIPPON PHARMACEUT CO LTD

JOURNAL
 OS Artificial gene
 OC Artificial sequence; Genes.
 PN JP 1993260987-A/19
 PD 12-OCT-1993
 PF 28-APR-1992 JP 1992136213
 PR 09-MAY-1991 JP 91P 135950
 PI YAMAGISHI JUNICHI, MATSUO TOKUYUKI, FUKUI JUICHI, PI YAMADA MASAAKI
 PC C12P21/02,C12N1/21//C12N15/12,(C12P21/02,C12R1:19),(C12N1/21,C12R1:19);
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC anti-sense: No.

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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 7.4e-57;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTTCACCAATAGGAAGTC 60
 DB 150 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTTCACCAATAGGAAGTC 209
 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCACAGCAGCAAGTGTCCCAAGAAGCT 120
 DB 210 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCACAGCAGCAAGTGTCCCAAGAAGCT 269
 QY 121 GTGATCTTCAAGACCATTTGGCCAGAGAGATCTGTCTGACCCCAAGCAGAGTGGGTT 180
 DB 270 GTGATCTTCAAGACCATTTGGCCAGAGAGATCTGTCTGACCCCAAGCAGAGTGGGTT 329
 QY 181 CAGGATTCATGGACCACTGGACAGCAACCACTCGAAGACT 228
 DB 330 CAGGATTCATGGACCACTGGACAGCAACCACTCGAAGACT 377

RESULT 7
 LOCUS E05599
 DEFINITION cDNA encoding monocyte chemotactic factor.
 ACCESSION E05599
 VERSION E05599.1 GI:2173786
 KEYWORDS JP 1993260987-A/3.
 SOURCE Escherichia coli
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE
 1 (bases 1 to 554)

Yamagishi,J., Matsuo,T., Fukui,J. and Yamada,M.
 PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYPEPTIDE AND MICROBIAL STRAIN PRODUCING THE POLYPEPTIDE
 Patent: JP 1993260987-A 3 12-OCT-1993;
 DAINIPPON PHARMACEUT CO LTD

COMMENT
 PN JP 1993260987-A/3
 PD 12-OCT-1993
 PF 28-APR-1992 JP 1992136213
 PR 09-MAY-1991 JP 91P 135950
 PI YAMAGISHI JUNICHI, MATSUO TOKUYUKI, FUKUI JUICHI, PI YAMADA MASAAKI
 PC C12P21/02,C12N1/21//C12N15/12,(C12P21/02,C12R1:19),(C12N1/21,C12R1:19);
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key
 FH Location/Qualifiers
 5'UTR 1..39
 FT RBS 22..29
 FT mat_peptide 40..267
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 CDS 40..270
 FT /product='monocyte chemotactic factor' FT
 3'UTR 271..554.
 Location/Qualifiers
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 /organism="Escherichia coli"
 /mol_type="genomic RNA"
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ORIGIN
 Query Match 100.0%; Score 228; DB 6; Length 554;
 Best Local Similarity 100.0%; Pred. No. 7.4e-57;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTTCACCAATAGGAAGTC 60
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 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCACAGCAGCAAGTGTCCCAAGAAGCT 120
 DB 100 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCACAGCAGCAAGTGTCCCAAGAAGCT 159
 QY 121 GTGATCTTCAAGACCATTTGGCCAGAGAGATCTGTCTGACCCCAAGCAGAGTGGGTT 180
 DB 160 GTGATCTTCAAGACCATTTGGCCAGAGAGATCTGTCTGACCCCAAGCAGAGTGGGTT 219
 QY 181 CAGGATTCATGGACCACTGGACAGCAACCACTCGAAGACT 228
 DB 220 CAGGATTCATGGACCACTGGACAGCAACCACTCGAAGACT 267

RESULT 8
 LOCUS AX698741
 DEFINITION Sequence 72 from Patent WO02063030.
 ACCESSION AX698741
 VERSION AX698741.1 GI:29499529
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE
 1
 Lyamichev,V., Skrzypczynski,Z., Allawi,H.T., Wayland,S.R., Takova,T. and Neri,B.P.
 Charge tags and separation of nucleic acid molecules
 Patent: WO 02063030-A 72 15-AUG-2002;
 THIRD WAVE TECHNOLOGIES, INC. (US)

JOURNAL
 Location/Qualifiers
 1..647
 /organism="synthetic construct"

ORIGIN

Query Match 100.0%; Score 228; DB 6; Length 647;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCAGTCTGTTTAACTTCAACATAGGAAGATC 60
DB 70 CAGCCAGATGCAATCAATGCCCCAGTCCAGTCTGTTTAACTTCAACATAGGAAGATC 129

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 130 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCCAGCAGCAAGTGTCCCAAGAAGCT 189

QY 121 GTGATCTTCAAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 190 GTGATCTTCAAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 249

QY 181 CAGGATTCATGACCACTGCGAAGCAAGCAAAACCCAACTCCGAAGACT 228
DB 250 CAGGATTCATGACCACTGCGAAGCAAGCAAAACCCAACTCCGAAGACT 297

RESULT 9
AR337874
LOCUS AR337874 725 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 3 from patent US 6569418.
ACCESSION AR337874
VERSION AR337874.1 GI:33724486
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 725)
AUTHORS Garzino-Demo, A. and DeVico, A. L.
TITLE Immuno-modulating effects of chemokines in DNA vaccination
JOURNAL Patent: US 6569418-A 3 27-MAY-2003;
FEATURES Location/Qualifiers
source 1..725
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 228; DB 6; Length 725;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCAGTCTGTTTAACTTCAACATAGGAAGATC 60
DB 123 CAGCCAGATGCAATCAATGCCCCAGTCCAGTCTGTTTAACTTCAACATAGGAAGATC 182

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 183 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCCAGCAGCAAGTGTCCCAAGAAGCT 242

QY 121 GTGATCTTCAAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 303 CAGGATTCATGACCACTGCGAAGCAAGCAAAACCCAACTCCGAAGACT 350

RESULT 10
AR380799
LOCUS AR380799 725 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1344 from patent US 6607879.
ACCESSION AR380799
VERSION AR380799.1 GI:40088433
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 725)
AUTHORS Cocks, B. G., Stuart, S. G. and Seilhamer, J. J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 1344 19-AUG-2003;
FEATURES Location/Qualifiers
source 1..725
/organism="unknown"
/mol_type="genomic DNA"

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Query Match 100.0%; Score 228; DB 6; Length 725;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCAGTCTGTTTAACTTCAACATAGGAAGATC 60
DB 123 CAGCCAGATGCAATCAATGCCCCAGTCCAGTCTGTTTAACTTCAACATAGGAAGATC 182

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 183 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCCAGCAGCAAGTGTCCCAAGAAGCT 242

QY 121 GTGATCTTCAAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 243 GTGATCTTCAAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 302

RESULT 11
AX774742
LOCUS AX774742 725 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 58 from Patent WO03038129.
ACCESSION AX774742
VERSION AX774742.1 GI:32486258
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Raponi, M.
TITLE Methods for assessing and treating leukemia
JOURNAL Patent: WO 03038129-A 58 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
FEATURES Location/Qualifiers
source 1..725
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match 100.0%; Score 228; DB 6; Length 725;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCAGTCTGTTTAACTTCAACATAGGAAGATC 60
DB 123 CAGCCAGATGCAATCAATGCCCCAGTCCAGTCTGTTTAACTTCAACATAGGAAGATC 182

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 183 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCCAGCAGCAAGTGTCCCAAGAAGCT 242

QY 121 GTGATCTTCAAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 243 GTGATCTTCAAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 302

181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228
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 303 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 350

RESULT 12
 HSMCP1
 LOCUS H.sapiens mRNA for monocyte chemoattractant protein 1 (MCP-1). 725 bp mRNA linear PRI 03-APR-1995
 DEFINITION
 ACCESSION X14768
 VERSION X14768.1 GI:34513
 KEYWORDS monocyte chemoattractant protein 1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 725)
 AUTHORS Yoshimura, T., Yuhki, N., Moore, S.K., Appella, E., Lerman, M.I. and Leonard, E.J.
 TITLE Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression in mitogen-stimulated blood mononuclear leukocytes, and sequence similarity to mouse competence gene JE
 JOURNAL FEBS Lett. 244 (2), 487-493 (1989)
 MEDLINE 89153605
 PUBMED 2465924
 COMMENT ZAP11.
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 1..725
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /codon_start=1
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 /protein_id="CAA32876.1"
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 /db_xref="GOA:P13500"
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 123..350
 /product="MCP-1 (AA 1 - 76)"
 162..170
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 707..712
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 725
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 Best Local Similarity 100.0%; Pred. No. 7.5e-57;
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 QY 1 CAGCCAGATGCAATCAATGCCCGACCTGCTGTATACCTCCCAATAGGAAGATC 60
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 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCACCAGCAAGTGTCCCAAGAAAGCT 120
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 Db 183 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCACCAGCAAGTGTCCCAAGAAAGCT 242
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 QY 121 GTGATCTTCAGACCATTTGCGCAAGAGAGATCTGTGTCACCCCAAGCAAGTGGGTT 180
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 Db 243 GTGATCTTCAGACCATTTGCGCAAGAGAGATCTGTGTCACCCCAAGCAAGTGGGTT 302
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 QY 181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228
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 Db 303 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 350
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RESULT 14
 S71513
 LOCUS monocyte chemoattractant protein-1 [human, mRNA, 739 nt]. 739 bp mRNA linear PRI 07-MAY-1993
 DEFINITION
 ACCESSION S71513
 VERSION S71513.1 GI:240867
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 739)
 AUTHORS Yoshimura, T. and Leonard, E.J.
 TITLE Human monocyte chemoattractant protein-1 (MCP-1)
 JOURNAL Adv. Exp. Med. Biol. 305, 47-56 (1991)
 MEDLINE 92095166
 PUBMED 1661560
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsg 71513] from the original journal article.
 This sequence comes from 2.
 FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"

Db 303 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 350
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RESULT 13
 AX577974
 LOCUS Sequence 96 from Patent WO02081745. 739 bp DNA linear PAT 08-JAN-2003
 DEFINITION
 ACCESSION AX577974
 VERSION AX577974.1 GI:27647182
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Garcia, T., roman Roman, S., Baron, R., Call, K., Theilhaber, J., Connolly, T., Jackson, A., Bushnell, S.E. and Rawadi, G.
 TITLE Genes involved in osteogenesis and methods of use
 JOURNAL Patent: WO 02081745-A 96 17-OCT-2002;
 Aventis Pharma S.A. (FR)
 FEATURES
 source Location/Qualifiers
 1..739
 /organism="Homo sapiens"
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 Best Local Similarity 100.0%; Pred. No. 7.5e-57;
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 QY 121 GTGATCTTCAGACCATTTGCGCAAGAGAGATCTGTGTCACCCCAAGCAAGTGGGTT 180
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 Db 243 GTGATCTTCAGACCATTTGCGCAAGAGAGATCTGTGTCACCCCAAGCAAGTGGGTT 302
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 QY 181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228
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 Db 303 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 350
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RESULT 14
 S71513
 LOCUS monocyte chemoattractant protein-1 [human, mRNA, 739 nt]. 739 bp mRNA linear PRI 07-MAY-1993
 DEFINITION
 ACCESSION S71513
 VERSION S71513.1 GI:240867
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 739)
 AUTHORS Yoshimura, T. and Leonard, E.J.
 TITLE Human monocyte chemoattractant protein-1 (MCP-1)
 JOURNAL Adv. Exp. Med. Biol. 305, 47-56 (1991)
 MEDLINE 92095166
 PUBMED 1661560
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsg 71513] from the original journal article.
 This sequence comes from 2.
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          /note="monocyte chemoattractant protein-1, MCP-1"
          /note="This sequence comes from 2, MCP-1"
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          /protein_id="AAB20651.1"
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          /translation="MKVSAALLCLLLIAATFIPQGLAOPDAINAPVTCYVNFNRRKIS
VORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKQVQDSMDHLDKQTQPKT"
ORIGIN
Query Match      100.0%; Score 228; DB 9; Length 739;
Best Local Similarity 100.0%; Pred. NO. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTATTAATTCACCAATAGGAGATC 198
Db 123 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTATTAATTCACCAATAGGAGATC 182
Qy 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCAACAGCAGCAAGTGTCCCAAGAAGCT 120
Db 183 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCAACAGCAGCAAGTGTCCCAAGAAGCT 242
Qy 121 GTGATCTTCAAGACCATTTGTGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 180
Db 243 GTGATCTTCAAGACCATTTGTGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 302
Qy 181 CAGGATTCATGGACCACTGGACAAGCAACCCAACTCCGAAGACT 228
Db 303 CAGGATTCATGGACCACTGGACAAGCAACCCAACTCCGAAGACT 350

RESULT 15
AL7786 LOCUS      741 bp mRNA linear PAT 30-SEP-1994
DEFINITION MCP-1 mRNA.
ACCESSION AL7786
VERSION AL7786.1 GI:641144
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 741)
AUTHORS     Caput,D., Ferrara,P., Miloux,B., Minty,A. and Vita,N.
TITLE       Protein with cytokine activity, recombinant DNA, expression vector
            and hosts for obtaining it
JOURNAL     Patent: EP 0488900-A 25 03-JUN-1992;
            ELF SANOFI
FEATURES
source      1..741
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            /db_xref="SWISS-PROT:P13500"
            /translation="MKVSAALLCLLLIAATFIPQGLAOPDAINAPVTCYVNFNRRKIS
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ORIGIN
Query Match      100.0%; Score 228; DB 6; Length 741;
Best Local Similarity 100.0%; Pred. NO. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTATTAATTCACCAATAGGAGATC 60
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Db 139 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTATTAATTCACCAATAGGAGATC 198
Qy 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCAACAGCAGCAAGTGTCCCAAGAAGCT 120
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Qy 181 CAGGATTCATGGACCACTGGACAAGCAACCCAACTCCGAAGACT 228
Db 319 CAGGATTCATGGACCACTGGACAAGCAACCCAACTCCGAAGACT 366
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Job time : 1394 secs

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OM nucleic - nucleic search, using sw model

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Title: 07330446

Perfect score: 228

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Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: Geneseq2001as:*
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6: Geneseq2002s:*
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8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 228 | 100.0 | 300 | 6 | ABL60575 Human mon |
| 3 | 228 | 100.0 | 300 | 7 | ACC42732 Monocyte |
| 4 | 228 | 100.0 | 475 | 6 | ABV97697 Human pan |
| 5 | 228 | 100.0 | 647 | 6 | ABs68800 Human mon |
| 6 | 228 | 100.0 | 725 | 2 | AAQ85370 Chemoattr |
| 7 | 228 | 100.0 | 725 | 2 | AAx8631 Monocyte |
| 8 | 228 | 100.0 | 725 | 9 | AAD58817 Human mon |
| 9 | 228 | 100.0 | 725 | 9 | ADD18494 Human pro |
| 10 | 228 | 100.0 | 725 | 9 | ADE84839 Farnesyl |
| 11 | 228 | 100.0 | 738 | 1 | AA91337 DNA which |
| 12 | 228 | 100.0 | 739 | 2 | AAV10341 cDNA enco |
| 13 | 228 | 100.0 | 739 | 6 | ABV78071 Hyptoxia-r |
| 14 | 228 | 100.0 | 739 | 6 | ABZ34738 Coding se |
| 15 | 228 | 100.0 | 741 | 3 | AAA34899 Human ade |
| 16 | 228 | 100.0 | 741 | 3 | AAF21021 Human low |
| 17 | 228 | 100.0 | 741 | 7 | ABZ96715 Human nuc |
| 18 | 228 | 100.0 | 757 | 9 | ADD14996 Human mon |
| 19 | 228 | 100.0 | 802 | 2 | AAZ33515 Human pro |
| 20 | 228 | 100.0 | 804 | 7 | ABX63583 Human CDN |
| 21 | 228 | 100.0 | 978 | 3 | AAZ61117 DNA enco |
| 22 | 228 | 100.0 | 984 | 3 | AAZ61118 DNA enco |
| 23 | 228 | 100.0 | 999 | 3 | AAZ61119 DNA enco |

| | | | | | | |
|----|-------|------|------|---|----------|-----------|
| 24 | 227.6 | 99.8 | 1712 | 2 | AAV34249 | Human sec |
| 25 | 227.6 | 99.8 | 1712 | 7 | ACD08120 | CDNA enco |
| 26 | 227.6 | 99.8 | 1822 | 2 | AAV34248 | Human sec |
| 27 | 227.6 | 99.8 | 1822 | 7 | ACD08119 | CDNA enco |
| 28 | 227.2 | 99.6 | 330 | 2 | AAQ05625 | Human MCF |
| 29 | 226.4 | 99.3 | 231 | 2 | AAQ03528 | Mature MC |
| 30 | 226.4 | 99.3 | 356 | 2 | AAV86200 | EST clone |
| 31 | 226.4 | 99.3 | 382 | 2 | AAV86197 | EST clone |
| 32 | 226.4 | 99.3 | 418 | 2 | AAQ30749 | MCF (Drai |
| 33 | 226.4 | 99.3 | 473 | 6 | ABV96715 | Human pan |
| 34 | 226.4 | 99.3 | 554 | 2 | AAQ30745 | MCF (SS) |
| 35 | 226.4 | 99.3 | 661 | 3 | AAA74882 | Human che |
| 36 | 226.4 | 99.3 | 741 | 2 | AAQ30748 | AAa74882 |
| 37 | 224.8 | 98.6 | 228 | 2 | AAQ48092 | Monocyte |
| 38 | 221.6 | 97.2 | 524 | 2 | AAQ30746 | MCF (DS) |
| 39 | 220.4 | 96.7 | 378 | 3 | AA44418 | Human sec |
| 40 | 211.2 | 92.6 | 361 | 2 | AAV86195 | EST clone |
| 41 | 205.2 | 90.0 | 279 | 6 | ABL60574 | Human mon |
| 42 | 205.2 | 90.0 | 279 | 7 | ACC42733 | Monocyte |
| 43 | 204 | 89.5 | 207 | 6 | ABA02498 | Human mut |
| 44 | 196 | 86.0 | 213 | 2 | AAZ24805 | Human mon |
| 45 | 193.2 | 84.7 | 338 | 2 | AAV88315 | EST clone |

ALIGNMENTS

RESULT 1

| | | |
|----|--|------------------------|
| ID | ABA02497 | standard; DNA; 228 BP. |
| XX | ABA02497; | |
| AC | ABA02497; | |
| XX | | |
| DT | 26-MAR-2002 | (first entry) |
| XX | | |
| DE | Human monocyte chemoattractant protein-1 (MCP-1) DNA. | |
| XX | | |
| KW | Human; monocyte chemoattractant protein-1; MCP-1; C-C chemokine family; | |
| KW | pulmonary hypertension; primary; hypotensive; gene; ds. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PH | Location/Qualifiers | |
| FT | 1..228 | |
| FT | /tag= a | |
| FT | /partial | |
| FT | /product= "Human MCP-1" | |
| FT | /note= "No start or stop codon given in the | |
| FT | specification" | |
| FT | replace(3..25, GG) | |
| FT | /tag= b | |
| FT | /note= "The sequence encoding the 7ND-MCP-1 mutant | |
| FT | (ABA02498) contains a 24 bp deletion relative to this | |
| FT | sequence" | |
| WT | WC200189582-A1. | |
| XX | | |
| PD | 29-NOV-2001. | |
| XX | | |
| PP | 25-MAY-2001; 2001WO-JP004381. | |
| XX | | |
| XX | 26-MAY-2000; 2000JP-00161145. | |
| XX | | |
| PA | (TAKE) TAKEDA CHEM IND LTD. | |
| PA | (EGAS/) EGASHIRA K. | |
| XX | | |
| XX | Egashira K, Yonemitsu Y, Sueishi K, Ikeda Y, Inada Y; | |
| DR | WPI; 2002-083059/11. | |
| DR | P-PSDB; AAM53048. | |
| XX | | |
| PT | Preventives and remedies for pulmonary hypertension containing mutant of | |
| PT | MCP-1 antagonistic inhibitory type or its salt, encoded DNA or | |

PT neutralization antibody.
XX Disclosure; Page 32; 39pp; Japanese.
XX The invention relates to preventives and remedies for pulmonary hypertension, comprising an antagonistic inhibitory mutant of monocyte chemoattractant protein-1 (MCP-1). DNA encoding the mutant MCP-1, or a neutralising antibody against MCP-1. MCP-1 is a member of the C-C chemokine family. The preventives and remedies have hypotensive activity and can be used in the prevention and treatment of pulmonary hypertension particularly pulmonary primary hypertension. The present sequence CC represents DNA encoding wild-type human MCP-1
XX Sequence 228 BP; 71 A; 62 C; 53 G; 42 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 228; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.4e-62;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATATACCTTACCAATAGGAAGATC 60
DB 1 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATATACCTTACCAATAGGAAGATC 60

QY 61 TCAGTGCAGAGGCTCGCAGGCTATAGAGAATCACCAGCAAGTGTCCAAAGAAGCT 120
DB 61 TCAGTGCAGAGGCTCGCAGGCTATAGAGAATCACCAGCAAGTGTCCAAAGAAGCT 120

QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180

QY 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 228
DB 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 228

RESULT 2
ABL60575
ID ABL60575 standard; DNA; 300 BP.
XX ABL60575;
AC ABL60575;
XX ABL60575;
DT 27-AUG-2002 (first entry)
XX Human monocyte chemoattractant protein-1 (MCP-1) related DNA.
DE Human monocyte chemoattractant protein-1 (MCP-1) related DNA.
KW MCP-1; hepatic disease; monocyte chemoattractant protein-1; liver;
KW fibrosis; cirrhosis; hepatotropic; human; ds.
XX Homo sapiens.
OS Homo sapiens.
XX WO200230464-A1.
PN WO200230464-A1.
XX 18-APR-2002.
PD 18-APR-2002.
XX 28-SEP-2001; 2001WO-JP008552.
PF 11-OCT-2000; 2000JP-00310604.
PR (DAUC) DAIICHI PHARM CO LTD.
PA (EGAS/) EGASHIRA K.
XX Egashira K, Takeshita A, Koyanagi M, Nakamura M, Nishida K;
PI WPI; 2002-394437/42.
XX Agents for treating hepatic diseases comprise a monocyte chemoattractant protein-1 function inhibitor.
PT protein-1 function inhibitor.
XX Disclosure; Page 10; 18pp; Japanese.
PS The invention provides agents for treating and preventing hepatic diseases. The agents contain a monocyte chemoattractant protein-1 (MCP-1)

CC function inhibitor as the active ingredient. The MCP-1 function inhibitors are useful in treating and preventing hepatic diseases such as liver fibrosis or liver cirrhosis. The present sequence represents a human MCP-1 related DNA sequence
XX Sequence 300 BP; 83 A; 88 C; 68 G; 61 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 228; DB 6; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.8e-62;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATATACCTTACCAATAGGAAGATC 60
DB 70 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATATACCTTACCAATAGGAAGATC 129

QY 61 TCAGTGCAGAGGCTCGCAGGCTATAGAGAATCACCAGCAAGTGTCCAAAGAAGCT 120
DB 130 TCAGTGCAGAGGCTCGCAGGCTATAGAGAATCACCAGCAAGTGTCCAAAGAAGCT 189

QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 190 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 249

QY 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 228
DB 250 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 297

RESULT 3
ACC42732
ID ACC42732 standard; DNA; 300 BP.
XX ACC42732;
AC ACC42732;
XX ACC42732;
DT 06-AUG-2003 (first entry)
XX Monocyte chemotactic protein 1, MCP-1, related sequence, SEQ ID 1.
DE Human; immunosuppressive; organ transplant rejection; arteriosclerosis; endothelial thickening; monocyte chemotactic protein 1; MCP-1; ds.
KW Homo sapiens.
OS Homo sapiens.
XX WO2003037376-A1.
PN WO2003037376-A1.
XX 08-MAY-2003.
PD 01-NOV-2002; 2002WO-JP011441.
PF 02-NOV-2001; 2001JP-00337861.
PR (EGAS/) EGASHIRA K.
XX Egashira K, Takeshita A, Sata M;
PI WPI; 2003-457365/43.
XX Prevention or treatment of organ transplant rejection, comprises using monocyte chemotactic protein 1 to inhibit endothelial thickening or arteriosclerosis of homograft or allograft blood vessels.
XX Claim 6; Page 13; 20pp; Japanese.
XX The present invention relates to a method for preventing or treating organ transplant rejection. The method comprises preventing arteriosclerosis or endothelial thickening in blood vessel autograft or CC allograft, post-transplant, using an agent which inhibits the function of monocyte chemotactic protein 1 (MCP-1). The present sequence was used to illustrate the method of the invention
XX Sequence 300 BP; 83 A; 88 C; 68 G; 61 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 228; DB 7; Length 300;
XX

| | |
|----------|---|
| CC | and stimulating an immune response. The polynucleotides can be used as |
| CC | probes or primers for nucleic acid hybridisation, in the design and |
| CC | preparation of ribozyme molecules for inhibiting expression of the tumour |
| CC | polypeptides and proteins in the tumour cells, in vaccines and for gene |
| CC | therapy. Note: The sequence data for this patent did not form part of the |
| CC | printed specification, but was obtained in electronic format directly |
| CC | from WIPO at ftp.wipo.int/pub/published_pct_sequences |
| XX | |
| SQ | Sequence 475 BP; 134 A; 90 C; 122 G; 129 T; 0 U; 0 Other; |
| | |
| | Query Match 100.0%; Score 228; DB 6; Length 475; |
| | Best Local Similarity 100.0%; Pred. No. 4.6e-62; |
| | Matches 228; Conservative 0; Mismatches 0; Indels 0; Caps 0; |
| | |
| QY | 1 CAGCGAGATGCACCAATCAATGCCCGCTCACCCTGCTTAACTTCACCAATAGGAAGATC 60 |
| Dd | 404 CAGCGAGATGCACCAATCAATGCCCGCTCACCCTGCTTAACTTCACCAATAGGAAGATC 345 |
| | |
| QY | 61 TCAGTGCGAGAGGCTCGGAGCTATAGAAGAAATCACGAGCAGCAAGTGTCCTCAAAGAAGCT 120 |
| Dd | 344 TCAGTGCGAGAGGCTCGGAGCTATAGAAGAAATCACGAGCAGCAAGTGTCCTCAAAGAAGCT 285 |
| | |
| QY | 121 GTGATCTTCAAGACCATTTGTGCCAAGGAGATCTGTGCTGACCCCAGCAGAGTAGTGGTT 180 |
| Dd | 284 GTGATCTTCAAGACCATTTGTGCCAAGGAGATCTGTGCTGACCCCAGCAGAGTAGTGGTT 225 |
| | |
| QY | 181 CAGGATTCCATGGACACCTCGGACCAAGCAAAACCCAAACTCCGAAGACT 228 |
| Dd | 224 CAGGATTCCATGGACACCTCGGACCAAGCAAAACCCAAACTCCGAAGACT 177 |
| | |
| RESULT 5 | |
| ABS68800 | |
| ID | ABS68800 standard; RNA; 647 BP. |
| XX | |
| AC | ABS68800; |
| XX | |
| DT | 20-NOV-2002 (first entry) |
| XX | |
| DE | Human monocyte chemoattractant protein-1 (hMCP-1) RNA. |
| KW | Phosphoramidite; INVADER assay cleavage reaction; PEN1; cleavase; |
| KW | nucleic acid separation; DNA polymerase; human; MCP-1; ubiquitin; |
| KX | monocyte chemoattractant protein-1; gene; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO200263030-A2. |
| PD | 15-AUG-2002. |
| XX | |
| PF | 06-FEB-2002; 2002WO-US003423. |
| XX | |
| PR | 06-FEB-2001; 2001US-00777430. |
| XX | |
| PA | (THIR-) THIRD WAVE TECHNOLOGIES INC. |
| XX | |
| PI | Lyanichev V, Skrzpczynski Z, Allawi HT, Wayland SR, Takova T; |
| PI | Neri BP; |
| XX | |
| DR | WPI; 2002-674850/72. |
| XX | |
| PT | Composition useful for e.g. separation of nucleic acids comprises a |
| PT | positively or neutrally charged phosphoramidite. |
| PS | |
| XX | Example 14; Page 194; 197pp; English. |
| XX | |
| CC | The invention relates to a composition comprising a positively or |
| CC | neutrally charged phosphoramidite. The composition is useful for |
| CC | separation of nucleic acid molecules. The composition is further useful |
| CC | for fractionation of specific nucleic acids by selective charge reversal |
| CC | useful in e.g. INVADER assay cleavage reactions; and in the synthesis of |
| CC | charge-balanced molecules. In the fractionation of nucleic acid |

DR WPI; 2003-278396/27.
 XX Characterizing prostate tissue comprises providing a prostate tissue
 PT sample from a subject and detecting the presence or absence of expression
 PT of hepsin, pim-1 or E2H2.
 XX
 PS Disclosure; SEQ ID NO 66; 297pp; English.
 XX
 CC This invention relates to a novel method of characterising prostate
 CC tissue in a subject and to compositions and methods for cancer
 CC diagnostics, including cancer markers, in particular prostate cancer.
 CC Prostate cancer (PCA) is a leading cause of male cancer-related death.
 CC Additional serum and tissue biomarkers would aid diagnosis. The invention
 CC may provide means of producing compounds with a cytostatic activity or
 CC allow the development of gene therapy. The methods of the invention
 CC useful for characterising prostate tissue in a subject, screening
 CC compounds, characterising inconclusive prostate biopsy tissue in a
 CC subject, detecting AMACR (alpha-methylacyl-coenzyme A racemase)
 CC expression in a bodily fluid, characterising tissue in a subject,
 CC diagnosing cancer in a subject and inhibiting the growth of cells. The
 CC present sequence is a DNA sequence which is preferably utilised in the
 CC method of the invention.
 XX
 SQ Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;

Query Match 100.0%; Score 228; DB 9; Length 725;
 Best Local Similarity 100.0%; Pred. No. 5.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCATAGGAAGATC 60
 DB 123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCATAGGAAGATC 182
 QY 61 TCAGTCAGAGGCTCGCGAGCTATAGAGATCAACAGCAGCAAGTGTCCCAAGAGCT 120
 DB 183 TCAGTCAGAGGCTCGCGAGCTATAGAGATCAACAGCAGCAAGTGTCCCAAGAGCT 242
 QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
 DB 243 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 302
 QY 181 CAGGATTCATGGACCACTGTGACAGCAACCCCAAACTCCGAAGACT 228
 DB 303 CAGGATTCATGGACCACTGTGACAGCAACCCCAAACTCCGAAGACT 350

RESULT 10
 ADE84839
 ID ADE84839 standard; DNA; 725 BP.
 AC ADE84839;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #58.
 XX ss; cytostatic; farnesyl transferase inhibitor; gene expression;
 KW quininone; leukemia; cancer.
 XX
 XX Homo sapiens.
 OS
 PN WO2003038129-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 30-OCT-2002; 2002WO-US034784.
 XX
 PR 30-OCT-2001; 2001US-0338997P.
 PR 30-OCT-2001; 2001US-0340081P.
 PR 30-OCT-2001; 2001US-0340938P.
 PR 30-OCT-2001; 2001US-0341012P.
 XX
 XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

XX Raponi M;
 XX
 DR WPI; 2003-513497/48.
 XX
 PT Determining whether a patient will respond to treatment with a farnesyl
 PT transferase inhibitor, by analyzing the expression of gene that is
 PT differentially modulated in the presence of the inhibitor.
 XX
 PS Disclosure; SEQ ID NO 58; 346pp; English.
 XX

CC The invention relates to a method of determining whether a patient will
 CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
 CC analyzing the expression of gene that is differentially modulated in the
 CC presence of an FTI. The method is useful for determining whether a
 CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-
 CC chlorophenyl)]-1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
 CC methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
 CC patient with leukemia with FTI if the analysis indicates that the patient
 CC will respond. This sequence corresponds to a gene whose expression may be
 CC modulated in the presence of FTI.

SQ Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
 Query Match 100.0%; Score 228; DB 9; Length 725;
 Best Local Similarity 100.0%; Pred. No. 5.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCATAGGAAGATC 60
 DB 123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCATAGGAAGATC 182
 QY 61 TCAGTCAGAGGCTCGCGAGCTATAGAGATCAACAGCAGCAAGTGTCCCAAGAGCT 120
 DB 183 TCAGTCAGAGGCTCGCGAGCTATAGAGATCAACAGCAGCAAGTGTCCCAAGAGCT 242
 QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
 DB 243 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 302
 QY 181 CAGGATTCATGGACCACTGTGACAGCAACCCCAAACTCCGAAGACT 228
 DB 303 CAGGATTCATGGACCACTGTGACAGCAACCCCAAACTCCGAAGACT 350

RESULT 11
 AAN91337
 ID AAN91337 standard; cDNA; 738 BP.
 XX
 AC AAN91337;
 XX
 XX 25-MAR-2003 (revised)
 DT 17-DEC-2001 (revised)
 DT 25-JUL-1989 (first entry)
 XX
 DE DNA which encodes human monocyte chemo-attractant peptide-1.
 XX Human monocyte chemo-attractant peptide; inflammatory disease; neoplasms;
 KW ss.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS 53..350
 FT /*tag= a
 FT mat_peptide 120..347
 FT /*tag= c
 FT polyA_signal /label= mature MCP-1
 FT 705..709
 FT /*tag= b
 XX
 PN USN7330446-N.

KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
 KW preeclampsia; atherosclerosis; inflammatory condition; wound healing;
 KW inflammation; erythropoiesis; hair loss; human; gene; ds.
 XX Homo sapiens.
 XX WO200246465-A2.
 XX 13-JUN-2002.
 XX 10-DEC-2001; 2001WO-GB005458.
 XX 08-DEC-2000; 2000GB-00030076.
 XX 08-FEB-2001; 2001GB-00003156.
 XX 25-OCT-2001; 2001GB-00025666.
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
 PI Rayner WN;
 XX WPI; 2002-627238/67.
 XX Identifying a gene involved in disease for treating hypoxia-regulated
 PT conditions, comprises comparing the transcriptome/proteome of two cell
 PT types under different conditions and identifying a differentially
 PT regulated gene.
 XX Claim 37; Page 399; 538pp; English.
 XX The present invention relates to methods for identifying genes and
 CC proteins that are implicated in a specific disease or physiological
 CC condition. The method comprises comparing the transcriptome/proteome of a
 CC specialised cell type implicated in a disease or condition with that of a
 CC second specialised cell type, under two experimental conditions, and
 CC identifying a gene that is differentially regulated in the two
 CC specialised cell types under experimental conditions. ABV7873-ABV78116
 CC and ABP65061-ABP65257 were identified using the methods of the invention.
 CC The coding sequences and proteins are useful for treating a disease in a
 CC patient, for manufacture of a medicament for treating hypoxia-regulated
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
 CC biological response to hypoxia conditions, or hypoxic-associated
 CC pathology in a patient. The coding sequences and proteins are also useful
 CC for monitoring the therapeutic treatment of a disease or physiological
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,
 CC retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss
 XX SQ Sequence 739 BP; 222 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
 Query Match 100.0%; Score 228; DB 6; Length 739;
 Best Local Similarity 100.0%; Pred. No. 5.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCATAAGGAAGATC 60
 DB 123 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCATAAGGAAGATC 182
 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGATCACCAGCAAGTGTCCCAAGAGACT 120
 DB 183 TCAGTGCAGAGCTCGCGAGCTATAGAGATCACCAGCAAGTGTCCCAAGAGACT 242
 QY 121 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGTCACCCCAAGCAGAGTGGGTT 180
 DB 243 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGTCACCCCAAGCAGAGTGGGTT 302
 QY 181 CAGGATTCATGGACCATCTGGACCAAGCAAAACCCAACTCCGAAGACT 228
 DB 303 CAGGATTCATGGACCATCTGGACCAAGCAAAACCCAACTCCGAAGACT 350
 RESULT 15
 AAA34899
 ID AAA34899 standard; DNA; 741 BP.
 XX AAA34899;
 XX 28-JUL-2000 (first entry)
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2588.

ABZ34738 standard; cDNA; 739 BP.
 ABZ34738;
 04-FEB-2003 (first entry)
 Coding sequence SEQ ID 96, downregulated in osteogenesis.
 Osteopathic; osteogenesis modulator; gene therapy; osteogenesis;
 osteoporosis; bone disease; downregulator; human; ss.
 Homo sapiens.
 WO200281745-A2.
 17-OCT-2002.
 05-APR-2002; 2002WO-IB002211.
 05-APR-2001; 2001US-0281400P.
 (AVET) AVENTIS PHARMA SA.
 Garcia T, Roman Roman S, Baron R, Call K, Theilhaber J;
 Connolly T, Jackson A, Bushnell SE, Rawadi G;
 WPI; 2003-058567/05.
 Novel isolated nucleic acid upregulated/downregulated in osteogenesis,
 useful for bone disease therapy in subject.
 Claim 27; Page 124-125; 237pp; English.
 The present invention relates to novel nucleotide sequences, which are
 differentially expressed in models of osteogenesis upon being put in
 contact with a stimulator of osteogenesis. The present sequence is one
 such sequence. This sequence can be used for diagnosing osteoporosis/bone
 disease in a patient, promoting osteogenesis and/or preventing
 osteoporosis/bone disease. The present sequence encodes a secreted
 CC protein
 SQ Sequence 739 BP; 222 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
 Query Match 100.0%; Score 228; DB 7; Length 739;
 Best Local Similarity 100.0%; Pred. No. 5.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCATAAGGAAGATC 60
 DB 123 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCATAAGGAAGATC 182
 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGATCACCAGCAAGTGTCCCAAGAGACT 120
 DB 183 TCAGTGCAGAGCTCGCGAGCTATAGAGATCACCAGCAAGTGTCCCAAGAGACT 242
 QY 121 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGTCACCCCAAGCAGAGTGGGTT 180
 DB 243 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGTCACCCCAAGCAGAGTGGGTT 302
 QY 181 CAGGATTCATGGACCATCTGGACCAAGCAAAACCCAACTCCGAAGACT 228
 DB 303 CAGGATTCATGGACCATCTGGACCAAGCAAAACCCAACTCCGAAGACT 350
 RESULT 15
 AAA34899
 ID AAA34899 standard; DNA; 741 BP.
 XX AAA34899;
 XX 28-JUL-2000 (first entry)
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2588.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 XX
 XX PD 24-FEB-2000.
 XX
 XX PF 03-AUG-1999; 99WO-US017712.
 XX
 XX PR 03-AUG-1998; 98US-0095212P.
 XX
 XX PA (UYEC-) UNIV EAST CAROLINA.
 XX
 XX PI Nyce JW;
 XX
 XX DR WPI; 2000-205971/18.
 XX
 XX PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 XX PS Disclosure; Page 761-762; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (CN) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The CN can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONS reduces side effects. The A-containing ONS break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONS from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 741 BP; 214 A; 173 C; 133 G; 221 T; 0 U; 0 Other;
 Query Match 100.0%; Score 228; DB 3; Length 741;
 Best Local Similarity 100.0%; Pred. No. 5.5e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTTTACTTCCACCAATAGGAGATC 60
 DB 139 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTTTAACTTCCACCAATAGGAGATC 198
 61 TCAGTGCAGAGGCTCGCAGGCTATAGAGAAATCACGACGACGACGAGTCCCAAGAAGCT 120
 DB 199 TCAGTGCAGAGGCTCGCAGGCTATAGAGAAATCACGACGACGACGAGTCCCAAGAAGCT 258

QY 121 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAAGTGGTT 180
 DB 259 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAAGTGGTT 318
 QY 181 CAGGATTCATGGACCACTTGTGGCCAAAGCAGCAAAACCCAACTCCGAGACT 228
 DB 319 CAGGATTCATGGACCACTTGTGGCCAAAGCAGCAAAACCCAACTCCGAGACT 366

Search completed: August 31, 2004, 02:58:29
 Job time : 241 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:49:11 ; Search time 54 Seconds
(without alignments)
2343.126 Million cell updates/sec

Title: 07330446

Perfect score: 228

Sequence: 1 cagccagatgcaatcaatgc.....aaacccaactccgaagact 228

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 228 | 100.0 | 725 | 4 | US-09-591-992-3 |
| 2 | 228 | 100.0 | 725 | 4 | US-09-023-655-1344 |
| 3 | 228 | 100.0 | 741 | 3 | US-07-927-391-25 |
| 4 | 228 | 100.0 | 741 | 4 | US-09-023-655-1165 |
| 5 | 227.6 | 99.8 | 1712 | 4 | US-09-148-545-106 |
| 6 | 227.6 | 99.8 | 1822 | 4 | US-09-148-545-105 |
| 7 | 226.4 | 99.3 | 231 | 5 | PCT-US95-00605-2 |
| 8 | 224.8 | 98.6 | 228 | 1 | US-08-250-958-3 |
| 9 | 217.4 | 95.4 | 752 | 6 | 5212073-1 |
| 10 | 196 | 86.0 | 213 | 4 | US-09-463-451-29 |
| 11 | 196 | 86.0 | 213 | 4 | US-09-463-451-30 |
| 12 | 148.2 | 65.0 | 228 | 3 | US-07-927-391-13 |
| 13 | 148.2 | 65.0 | 810 | 4 | US-09-016-434-1273 |
| 14 | 148.2 | 65.0 | 814 | 3 | US-07-927-391-15 |
| 15 | 147.2 | 64.6 | 247 | 3 | US-07-927-391-17 |
| 16 | 139.6 | 61.2 | 294 | 4 | US-09-023-655-901 |
| 17 | 139.6 | 61.2 | 605 | 4 | US-09-366-887A-26 |
| 18 | 139.6 | 61.2 | 807 | 4 | US-09-023-655-978 |
| 19 | 139 | 61.0 | 840 | 4 | US-09-016-434-1033 |
| 20 | 138 | 60.5 | 813 | 4 | US-09-016-434-1156 |
| 21 | 135.4 | 59.4 | 207 | 4 | US-09-463-458A-28 |
| 22 | 135 | 59.2 | 315 | 3 | US-08-744-419-3 |
| 23 | 135 | 59.2 | 514 | 4 | US-09-545-894-3 |
| 24 | 135 | 59.2 | 540 | 3 | US-08-744-419-1 |
| 25 | 134.4 | 58.9 | 207 | 4 | US-09-463-458A-8 |
| 26 | 134.4 | 58.9 | 207 | 4 | US-09-463-458A-25 |
| 27 | 127.2 | 55.8 | 400 | 4 | US-09-833-381-1234 |

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|----|-------|------|------|---|--------------------|--------------------|
| 28 | 125.6 | 55.1 | 297 | 3 | US-08-613-822-3 | Sequence 3, Appli |
| 29 | 125.6 | 55.1 | 297 | 3 | US-08-852-212-1 | Sequence 1, Appli |
| 30 | 125.6 | 55.1 | 297 | 4 | US-09-479-729B-3 | Sequence 3, Appli |
| 31 | 125.6 | 55.1 | 297 | 4 | US-09-261-201A-3 | Sequence 3, Appli |
| 32 | 125.6 | 55.1 | 297 | 4 | US-09-717-209-3 | Sequence 3, Appli |
| 33 | 125.6 | 55.1 | 802 | 4 | US-09-016-434-687 | Sequence 687, App |
| 34 | 125.6 | 55.1 | 823 | 4 | US-09-545-894-1 | Sequence 1, Appli |
| 35 | 111 | 48.7 | 818 | 4 | US-09-366-887A-15 | Sequence 15, Appli |
| 36 | 109.6 | 48.1 | 994 | 4 | US-09-366-887A-5 | Sequence 5, Appli |
| 37 | 99.2 | 43.5 | 1047 | 4 | US-09-546-028-44 | Sequence 44, Appli |
| 38 | 99.2 | 43.5 | 1080 | 4 | US-09-546-028-39 | Sequence 39, Appli |
| 39 | 99.2 | 43.5 | 1086 | 4 | US-09-546-028-37 | Sequence 37, Appli |
| 40 | 99.2 | 43.5 | 1113 | 4 | US-09-546-028-38 | Sequence 38, Appli |
| 41 | 99.2 | 43.5 | 1805 | 4 | US-09-546-028-45 | Sequence 45, Appli |
| 42 | 95.2 | 41.8 | 121 | 4 | US-09-463-458A-4 | Sequence 4, Appli |
| 43 | 88 | 38.6 | 272 | 4 | US-09-023-655-845 | Sequence 845, App |
| 44 | 86.8 | 38.1 | 253 | 4 | US-09-833-381-1229 | Sequence 1229, Ap |
| 45 | 72 | 31.6 | 353 | 4 | US-09-366-887A-21 | Sequence 21, Appli |

ALIGNMENTS

RESULT 1

US-09-591-992-3

; Sequence 3, Application US/09591992

; Patent No. 6569418

; GENERAL INFORMATION:

; APPLICANT: Gallo, Robert C.

; APPLICANT: Devico, Anthony L.

; APPLICANT: Garzino, Alfredo

; TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination

; FILE REFERENCE: 4115-109 CIP

; CURRENT APPLICATION NUMBER: US/09/591,992

; CURRENT FILING DATE: 2000-06-12

; PRIOR APPLICATION NUMBER: PCT/US98/26291

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/186,416

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 60/069,281

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 725

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-591-992-3

Query Match 100.0%; Score 228; DB 4; Length 725;
Best Local Similarity 100.0%; Pred.No. 3.8e-61; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0

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| Qy | 1 | CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTTTATTAACCTCCCAATAGGAATC | 60 |
| Db | 123 | CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTTTATTAACCTCCCAATAGGAATC | 182 |
| Qy | 61 | TCAGTCGAGGGTCGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT | 120 |
| Db | 183 | TCAGTCGAGGGTCGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT | 242 |
| Qy | 121 | GTGATCTTCAAGACCAATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT | 180 |
| Db | 243 | GTGATCTTCAAGACCAATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT | 302 |
| Qy | 181 | CAGATTCCATGGACCACTGGACAGCAAAACCCAACTCCGAAGACT | 228 |
| Db | 303 | CAGATTCCATGGACCACTGGACAGCAAAACCCAACTCCGAAGACT | 350 |

RESULT 2

US-09-023-655-1344

; Sequence 1344, Application US/09023655

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/ Patent No. 6607879
/ GENERAL INFORMATION:
/ APPLICANT: COCKS, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffery J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ TITLE OF INVENTION: EXPRESSION
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION NUMBER:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1344:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 725 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: G34513
/ US-09-023-655-1344

Query Match 100.0%; Score 228; DB 4; Length 725;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCCAGTCACTGCTGTATATACCTTCCACCAATAGGAAGATC 60
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QY 61 TCAGTGCAGAGCTGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 183 TCAGTGCAGAGCTGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 242
QY 121 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 243 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 302
QY 181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228
DB 303 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 350

RESULT 3
US-09-927-391-25
; Sequence 25, Application US/07927391
; Patent No. 6001649
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel

/ Patent No. 6607879
/ GENERAL INFORMATION:
/ APPLICANT: COCKS, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffery J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ TITLE OF INVENTION: EXPRESSION
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION NUMBER:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1344:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 725 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: G34513
/ US-09-023-655-1344

Query Match 100.0%; Score 228; DB 4; Length 725;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCCAGTCACTGCTGTATATACCTTCCACCAATAGGAAGATC 60
DB 123 CAGCCAGATGCAATCAATGCCCCCAGTCACTGCTGTATATACCTTCCACCAATAGGAAGATC 182
QY 61 TCAGTGCAGAGCTGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 183 TCAGTGCAGAGCTGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 242
QY 121 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 243 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 302
QY 181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228
DB 303 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 350

RESULT 3
US-09-927-391-25
; Sequence 25, Application US/07927391
; Patent No. 6001649
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel

/ Patent No. 6607879
/ GENERAL INFORMATION:
/ APPLICANT: COCKS, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffery J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ TITLE OF INVENTION: EXPRESSION
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION NUMBER:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1344:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 725 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: G34513
/ US-09-023-655-1344

Query Match 100.0%; Score 228; DB 3; Length 741;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCCAGTCACTGCTGTATATACCTTCCACCAATAGGAAGATC 60
DB 139 CAGCCAGATGCAATCAATGCCCCCAGTCACTGCTGTATATACCTTCCACCAATAGGAAGATC 198
QY 61 TCAGTGCAGAGCTGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 199 TCAGTGCAGAGCTGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 258
QY 121 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 259 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 318
QY 181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228
DB 319 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 366

RESULT 4
US-09-023-655-1165
; Sequence 1165, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: COCKS, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffery J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
```

NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0855
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G187434
US-09-023-655-1165

Query Match 100.0%; Score 228; DB 4; Length 741;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGATGCAATCAATGCCCGATCACCCTGCTGTATTAATCTTCAACAATAGGAATC 60
DB 139 CAGCAGATGCAATCAATGCCCGATCACCCTGCTGTATTAATCTTCAACAATAGGAATC 198

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QY 181 CAGATTCTCAGACCACTGAGCAGCAAAACCCAACTCGAAGACT 228
DB 319 CAGATTCTCAGACCACTGAGCAGCAAAACCCAACTCGAAGACT 366

RESULT 5
US-09-148-545-106
Sequence 106, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001PI
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162

EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
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EARLIER APPLICATION NUMBER: 60/047,502
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EARLIER APPLICATION NUMBER: 60/047,618
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EARLIER APPLICATION NUMBER: 60/047,503
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EARLIER APPLICATION NUMBER: 60/047,581
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EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
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EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
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EARLIER FILING DATE: 1997-04-11

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EARLIER APPLICATION NUMBER: 60/043,672
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EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 05-Sep-1997
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 106
LENGTH: 1712

Query Match 99.8%; Score 227.6; DB 4; Length 1712;
Best Local Similarity 99.6%; Pred. No. 6.9e-61;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTCCACCTGCTGTATTAACCTCCCAATAGGAAGATC 60
Db 1059 CAGCCAGATGCAATCAATGCCCGAGTCCACCTGCTGTATTAACCTCCCAATAGGAAGATC 1118

QY 61 TCAGTCAGAGGCTCGGAGCTATAGAGATCAGCAGCAGCAAGTGTCCCAAGAGCT 120
Db 1119 TCAGTCAGAGGCTCGGAGCTATAGAGATCAGCAGCAGCAAGTGTCCCAAGAGCT 1178

QY 121 GTGATCTTCAAGACCATTTGGCCAGAGAGATCTGTGTGACCCCAAGCAGAGTGGGTT 180
Db 1179 GTGATCTTCAAGACCATTTGGCCAGAGAGATCTGTGTGACCCCAAGCAGAGTGGGTT 1238

QY 181 CAGGATTCATGAGCACCCTTGACAGCAAGCAAAACCCAAACTCCGAAGCT 228
Db 1239 CAGGATTCATGAGCACCCTTGACAGCAAGCAAAACCCAAACTCCGAAGCT 1286

RESULT 6
US-09-148-545-105
Sequence 105, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1

[illegible]

EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
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EARLIER APPLICATION NUMBER: 60/056,881
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EARLIER APPLICATION NUMBER: 60/056,909
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 1822

Query Match 99.8%; Score 227.6; DB 4; Length 1822;
Best Local Similarity 99.6%; Pred. No. 7e-61;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGCCAGTCCCTGCTGTATTAACCTCACCATAAGAGATC 60
Db 1169 CAGCCAGATGCAATCAATGCCCGCCAGTCCCTGCTGTATTAACCTCACCATAAGAGATC 1228
QY 61 TCAGTGCAGAGCTCGGAGCTATAGAGATACACGAGCAAGTGTCCCAAGAGCT 120
Db 1229 TCAGTGCAGAGCTCGGAGCTATAGAGATACACGAGCAAGTGTCCCAAGAGCT 1288
QY 121 GTGATCTTCAAGACATTTGGCCAGAGATCTGTCTGACCCCGAGAGAGTGGTT 180
Db 1289 GTGATCTTCAAGACATTTGGCCAGAGATCTGTCTGACCCCGAGAGAGTGGTT 1348
QY 181 CAGGATTCATGGACCACTGGACAAACCAACCAACTCCGAGACT 228
Db 1349 CAGGATTCATGGACCACTGGACAAACCAACCAACTCCGAGACT 1396

RESULT 7
US-0595-00605-2
; Sequence 2, Application PC/TUS9500605

GENERAL INFORMATION:
APPLICANT: Lyle, Leon
TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING
TITLE OF INVENTION: VASCULAR RESTENOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mallinckrodt Medical, Inc.
STREET: 675 McDonnell Boulevard, P.O. Box 5840
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00605
FILING DATE: 13-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,917
FILING DATE: 14-JAN-1994
APPLICATION NUMBER: US 07/965,678
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vacca, Rita D.
REGISTRATION NUMBER: 33,624
REFERENCE/DOCKET NUMBER: 0783.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-895-7215
TELEFAX: 314-895-2156
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Monocyte Chemotactic Protein-1
STRAIN: human
PCT-US95-00605-2

Query Match 99.3%; Score 226.4; DB 5; Length 231;
Best Local Similarity 81.1%; Pred. No. 7.7e-61;
Matches 185; Conservative 42; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGCCAGTCCCTGCTGTATTAACCTCACCATAAGAGATC 60
Db 4 CAGCCAGATGCAATCAATGCCCGCCAGTCCCTGCTGTATTAACCTCACCATAAGAGATC 63
QY 61 TCAGTGCAGAGCTCGGAGCTATAGAGATACACGAGCAAGTGTCCCAAGAGCT 120
Db 64 UCAGUGCAGAGCTCGGAGCTATAGAGATACACGAGCAAGTGTCCCAAGAGCT 123
QY 121 GTGATCTTCAAGACATTTGGCCAGAGATCTGTCTGACCCCGAGAGAGTGGTT 180
Db 124 GUGAUUUCAGACCAUUGUGCCAGGAGUGUGUGUGUGUGUGUGUGUGUGUGUGUG 183
QY 181 CAGGATTCATGGACCACTGGACAAACCAACCAACTCCGAGACT 228
Db 184 CAGGAUUCUUGAGGACCACTGGACAAACCAACCAACTCCGAGACT 231

RESULT 8
US-08-250-958-3
; Sequence 3, Application US/08250958
; Patent No. 5571713

```

; GENERAL INFORMATION:
; APPLICANT: LYLE, LEON R.
; APPLICANT: KUNKEL, STEVEN L.
; APPLICANT: STRIETER, ROBERT M.
; TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING
; TITLE OF INVENTION: VASCULAR RESTENOSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,958
; FILING DATE: 27-MAY-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,678
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 2077-206A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-250-958-3

Query Match 98.6%; Score 224.8; DB 1; Length 228;
Best Local Similarity 80.7%; Pred. No. 2.4e-60;
Matches 184; Conservative 42; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCACATAGGAAGTC 60
Db 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCACATAGGAAGTC 60
Qy 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Qy 121 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 180
Db 121 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 180
Qy 181 CAGGATTCATGACCACTGACAGCAAAACCCAAACT 228
Db 181 CAGGATTCATGACCACTGACAGCAAAACCCAAACT 228

RESULT 9
5212073-1
; Patent No. 5212073
; APPLICANT: ROLLINS, BARRETT;STILES, CHARLES;WONG, GORDON G.
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/351,008

; FILING DATE: 12-MAY-1989
; SEQ ID NO: 1:
; LENGTH: 752
; 5212073-1

Query Match 95.4%; Score 217.4; DB 6; Length 752;
Best Local Similarity 99.5%; Pred. No. 7.2e-58;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCACATAGGAAGTC 60
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Qy 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db 202 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 261
Qy 121 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 180
Db 262 GTGATCTTCAAGACCATTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 321
Qy 181 CAGGATTCATGACCACTGACAGCAAAACCCAAACT 219
Db 322 CAGGATTCATGACCACTGACAGCAAAACCCAAACT 360

RESULT 10
US-09-463-451-29
; Sequence 29, Application US/09463451
; Patent No. 6537779
; GENERAL INFORMATION:
; APPLICANT: KARA, Bupendra V.
; PIOLI, David
; BUNDELL, Kenneth R.
; HOCKNEY, Robert C.
; TITLE OF INVENTION: T7 Promoter-Based Expression System
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/463,451
; FILING DATE: 03-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/02175
; FILING DATE: 21-JUL-1998
; APPLICATION NUMBER: GB 9715660.8
; FILING DATE: 25-JUL-1997
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-463-451-29

Query Match 86.0%; Score 196; DB 4; Length 213;
Best Local Similarity 97.5%; Pred. No. 1.9e-51;
Matches 199; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 25 GTCACCTGCTGTATTAACCTCACCACATAGGAAGATCTCAGTCAGAGGCTCGGAGCTAT 84
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Db 4 GTTACTGCTGTTATTAATCTTACCAACCGTAAATCTCAGTGCAGAGGCTCGGAGCTAT 63
QY 85 AGAAGATCACAGCAGCAGAGTGTCCAAAGAGCTGTGATCTTCAAGACCATTTGTGGCC 144
Db 64 AGAAGATCACAGCAGCAGAGTGTCCAAAGAGCTGTGATCTTCAAGACCATTTGTGGCC 123
QY 145 AAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTTTCAGGATTCATCGACACCATGGAC 204
Db 124 AAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTTTCAGGATTCATCGACACCATGGAC 183
QY 205 AAGCAAAACCAAACTCCGAAGACT 228
Db 184 AAGCAAAACCAAACTCCGAAGACT 207

RESULT 11

US-09-463-451-30/c
; Sequence 30, Application US/09463451
; Patent No. 653779
; GENERAL INFORMATION:
; APPLICANT: KARA, Bupendra V.
; PIOLI, David
; BUNDELL, Kenneth R.
; HOCKNEY, Robert C.
; TITLE OF INVENTION: T7 Promoter-Based Expression System
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/463,451
; FILING DATE: 03-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/02175
; FILING DATE: 21-JUL-1998
; APPLICATION NUMBER: GB 9715660.8
; FILING DATE: 25-JUL-1997

; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-463-451-30

Query Match 86.0%; Score 196; DB 4; Length 213;
Best Local Similarity 97.5%; Pred. No. 1.9e-51;
Matches 199; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 25 GTCACCTGCTGTTATTAATCTTACCAATAGGAAGATCTCAGTGCAGAGGCTCGGAGCTAT 84
Db 210 GTTACTGCTGTTATTAATCTTACCAACCGTAAATCTCAGTGCAGAGGCTCGGAGCTAT 151
QY 85 AGAAGATCACAGCAGCAGAGTGTCCAAAGAGCTGTGATCTTCAAGACCATTTGTGGCC 144
Db 150 AGAAGATCACAGCAGCAGAGTGTCCAAAGAGCTGTGATCTTCAAGACCATTTGTGGCC 91
QY 145 AAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTTTCAGGATTCATCGACACCATGGAC 204
Db 90 AAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTTTCAGGATTCATCGACACCATGGAC 31

QY 205 AAGCAAAACCAAACTCCGAAGACT 228
Db 30 AAGCAAAACCAAACTCCGAAGACT 7

RESULT 12

US-07-927-391-13
; Sequence 13, Application US/07927391
; Patent No. 6001649
; GENERAL INFORMATION:
; APPLICANT: CAFUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: MILOUX, Brigitte
; APPLICANT: MINTY, Adrian
; APPLICANT: VITA, Natalio
; TITLE OF INVENTION: Protein having a cytokin type
; TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/927,391
; FILING DATE: 19920929
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-07-927-391-13

Query Match 65.0%; Score 148.2; DB 3; Length 228;
Best Local Similarity 78.7%; Pred. No. 1.1e-36;
Matches 177; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCCGCAGTCCCTGCTGTTATACTTCACTCAAGAGATC 60
Db 1 CAGCCAGTGGGATTAATCTCAACTACCTGCTGCTACAGATTTATCAATAAGAAATC 60
QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTCCCAAGAGACT 120
Db 61 CTTAAGCAGAGGCTGGAGAGCTACAGAAGGACCCAGTAGCCACTGTCCCGGAGACT 120
QY 121 GTGATCTTCAAGACCATTTGTGCCAAGGAGATCTGTGTGACCCCAAGCAAGAGTGGTT 180
Db 121 GTAACTTTCAAGACCAAACTGGACAAGGAGATCTGTGCTGACCCCAAGCAAGAGTGGTGC 180
QY 181 CAGGATTCATCGACCTCGCAGCAGCAACCCCAACTCCGAG 225

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 02:59:34 ; Search time 254 Seconds

(without alignments)
4417.658 Million cell updates/sec

Title: 07330446

Perfect score: 228

Sequence: 1 cagccagatcaatcaatgc.....aaacccaactccgaagact 228

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Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 228 | 100.0 | 228 | 15 | US-10-276-971-3 |
| 2 | 228 | 100.0 | 294 | 13 | US-10-449-831A-209 |
| 3 | 228 | 100.0 | 405 | 13 | US-10-449-831A-213 |
| 4 | 228 | 100.0 | 475 | 15 | US-10-060-036-3105 |
| 5 | 228 | 100.0 | 647 | 9 | US-09-777-430A-72 |
| 6 | 228 | 100.0 | 725 | 15 | US-10-210-120-66 |
| 7 | 228 | 100.0 | 725 | 17 | US-10-641-643-1344 |
| 8 | 228 | 100.0 | 725 | 17 | US-10-283-975A-58 |
| 9 | 228 | 100.0 | 725 | 17 | US-10-764-649-17 |
| 10 | 228 | 100.0 | 739 | 13 | US-10-342-887-849 |
| 11 | 228 | 100.0 | 739 | 13 | US-10-172-118-849 |
| 12 | 228 | 100.0 | 739 | 13 | US-10-170-385-396 |
| 13 | 228 | 100.0 | 741 | 17 | US-10-641-643-1165 |
| 14 | 228 | 100.0 | 756 | 15 | US-10-133-013-210 |

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15 228 100.0 757 13 US-10-388-360-377 Sequence 377, Appl
16 228 100.0 757 15 US-10-339-778-1 Sequence 1, Appli
17 228 100.0 783 15 US-10-133-013-209 Sequence 209, App
18 228 100.0 804 10 US-09-971-429B-18 Sequence 18, Appl
19 228 100.0 804 14 US-10-044-090-583 Sequence 583, App
20 228 100.0 978 9 US-09-792-793A-52 Sequence 52, Appl
21 228 100.0 978 16 US-10-375-209A-52 Sequence 52, Appl
22 228 100.0 984 9 US-09-792-793A-53 Sequence 53, Appl
23 228 100.0 984 16 US-10-375-209A-53 Sequence 53, Appl
24 228 100.0 999 9 US-09-792-793A-54 Sequence 54, Appl
25 228 100.0 999 16 US-10-375-209A-54 Sequence 54, Appl
26 228 100.0 1102 15 US-10-198-846-9822 Sequence 9822, Ap
27 227.6 99.8 1712 9 US-09-981-876-106 Sequence 106, App
28 227.6 99.8 1712 10 US-09-148-545-106 Sequence 106, App
29 227.6 99.8 1822 9 US-09-981-876-105 Sequence 105, App
30 227.6 99.8 1822 10 US-09-148-545-105 Sequence 105, App
31 226.4 99.3 473 15 US-10-060-036-2123 Sequence 2123, Ap
32 226.4 99.3 661 17 US-10-778-827-104 Sequence 104, App
33 226.4 99.3 661 8 US-08-927-939-76 Sequence 76, Appl
34 204 89.5 207 15 US-10-276-971-4 Sequence 4, Appli
35 202 88.6 276 13 US-10-424-599-120461 Sequence 120461,
36 193.2 84.7 338 14 US-10-040-739-793 Sequence 793, A
37 189.6 83.2 384 13 US-10-085-783A-52639 Sequence 52639, A
38 189.6 83.2 384 16 US-10-242-535A-52639 Sequence 52639, A
c 39 173 75.9 1005 15 US-10-133-013-211 Sequence 211, App
40 159.6 70.0 724 14 US-10-044-090-839 Sequence 839, App
41 148.2 65.0 810 13 US-10-170-385-464 Sequence 464, App
42 148.2 65.0 810 16 US-10-305-720-1273 Sequence 1273, Ap
43 148.2 65.0 817 14 US-10-044-090-837 Sequence 837, App
44 148.2 65.0 1085 8 US-08-927-939-81 Sequence 81, Appl
45 148.2 65.0 1085 17 US-10-717-597-95 Sequence 95, Appl
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ALIGNMENTS

RESULT 1

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US-10-276-971-3
; Sequence 3, Application US/10276971
; Publication No. US20030162737A1
; GENERAL INFORMATION:
; APPLICANT: Egashira Kensuke
; APPLICANT: Yoshikazu Yonemitsu
; APPLICANT: Katsuo Sueishi
; APPLICANT: Yasuhiro Ikeda
; APPLICANT: Yoshiyuki Inada
; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
; FILE REFERENCE: 2733 USOP
; CURRENT APPLICATION NUMBER: US/10/276,971
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Human
US-10-276-971-3
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Query Match 100.0%; Score 228; DB 15; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.4e-66;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGATCAATCAATGCCAGTCCAGTCACTGCTGTATTAACCTCACCATTAGGAATC 60
Db 1 CAGCCAGATCAATCAATGCCAGTCCAGTCACTGCTGTATTAACCTCACCATTAGGAATC 60

Qy 61 TCAGTGCAGAGGTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAAGAGCT 120
Db 61 TCAGTGCAGAGGTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAAGAGCT 120

Qy 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
Db 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
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; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Allawi, Hatim T.
; APPLICANT: Wayland, Sarah R.
; APPLICANT: Takova, Tsetska
; APPLICANT: Neir, Bruce P.
; TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
; FILE REFERENCES: FORS-04912
; CURRENT APPLICATION NUMBER: US/09/777,430A
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 647
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-777-430A-72

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QY 121 GTGATCTTCAAGACCACTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 180
Db 243 GTGATCTTCAAGACCACTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 302

QY 181 CAGGATTCATGGACCACTGTGACACGACCAACCCAACTCCGAAGACT 228
Db 303 CAGGATTCATGGACCACTGTGACACGACCAACCCAACTCCGAAGACT 350

RESULT 8
US-10-283-975A-58
; Sequence 58, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 58
; LENGTH: 725
; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-58

Query Match 100.0%; Score 228; DB 17; Length 725;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAAGATC 60
Db 123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAAGATC 182

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCGACGAAAGTGTCCCAAGAAAGCT 120
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QY 121 GTGATCTTCAAGACCACTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 180
Db 243 GTGATCTTCAAGACCACTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 302

QY 181 CAGGATTCATGGACCACTGTGACACGACCAACCCAACTCCGAAGACT 228
Db 303 CAGGATTCATGGACCACTGTGACACGACCAACCCAACTCCGAAGACT 350

RESULT 9
US-10-764-649-17
; Sequence 17, Application US/10764649
; Publication No. US20040157253A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; APPLICANT: Chen, Hong
; APPLICANT: Barnes, Glenn
; TITLE OF INVENTION: INFLAMMATORY PROTEINS IN THE DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: METABOLIC DISORDERS
; FILE REFERENCE: MPI2003-025PIRNM
; CURRENT APPLICATION NUMBER: US/10/764,649
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/446041
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 20

QY 121 GTGATCTTCAAGACCACTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 180
Db 243 GTGATCTTCAAGACCACTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 302

QY 181 CAGGATTCATGGACCACTGTGACACGACCAACCCAACTCCGAAGACT 228
Db 303 CAGGATTCATGGACCACTGTGACACGACCAACCCAACTCCGAAGACT 350

RESULT 9
US-10-764-649-17
; Sequence 17, Application US/10764649
; Publication No. US20040157253A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; APPLICANT: Chen, Hong
; APPLICANT: Barnes, Glenn
; TITLE OF INVENTION: INFLAMMATORY PROTEINS IN THE DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: METABOLIC DISORDERS
; FILE REFERENCE: MPI2003-025PIRNM
; CURRENT APPLICATION NUMBER: US/10/764,649
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/446041
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 20
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; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 725
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)...(353)
US-10-764-649-17

Query Match 100.0%; Score 228; DB 17; Length 725;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAAGATC 60
Db 123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAAGATC 182

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCGACGAAAGTGTCCCAAGAAAGCT 120
Db 183 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCGACGAAAGTGTCCCAAGAAAGCT 242

QY 121 GTGATCTTCAAGACCACTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 180
Db 243 GTGATCTTCAAGACCACTTGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 302

QY 181 CAGGATTCATGGACCACTGTGACACGACCAACCCAACTCCGAAGACT 228
Db 303 CAGGATTCATGGACCACTGTGACACGACCAACCCAACTCCGAAGACT 350

RESULT 10
US-10-342-887-849
; Sequence 849, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 849
; LENGTH: 739
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-849

Query Match 100.0%; Score 228; DB 13; Length 739;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAAGATC 60
Db 123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAAGATC 182

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCGACGAAAGTGTCCCAAGAAAGCT 120
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RESULI 12
US-10-170-385-396
; Sequence 396, Application US/10170395
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Taylor, Stuart
; APPLICANT: Kingsman, Susan Mary

```

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G187434
SEQUENCE DESCRIPTION: SEQ ID NO: 1165 :
US-10-641-643-1165

Query Match 100.0%; Score 228; DB 17; Length 741;
Best Local Similarity 100.0%; Pred. No. 1e-65; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAATAGGAAGATC 60
DB 139 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAATAGGAAGATC 198
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 199 TCAGTGCAGAGGCTCGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 258
QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAGTGGGTT 180
DB 259 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAGTGGGTT 318
QY 181 CAGGATTCATGGACCACTTGACCAAGCAAAACCCAAATCCGAAGACT 228
DB 319 CAGGATTCATGGACCACTTGACCAAGCAAAACCCAAATCCGAAGACT 366

RESULT 14
US-10-133-013-210
; Sequence 210, Application US/10133013
; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 210
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 470784cB1
US-10-133-013-210

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Best Local Similarity 100.0%; Pred. No. 1e-65; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAATAGGAAGATC 60
DB 142 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAATAGGAAGATC 201
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 202 TCAGTGCAGAGGCTCGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 261
QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAGTGGGTT 180

DB 262 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAGTGGGTT 321
QY 181 CAGGATTCATGGACCACTTGACCAAGCAAAACCCAAATCCGAAGACT 228
DB 322 CAGGATTCATGGACCACTTGACCAAGCAAAACCCAAATCCGAAGACT 369

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US-10-388-360-377
; Sequence 377, Application US/10388360
; Publication No. US2003022528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 377
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-377

Query Match 100.0%; Score 228; DB 13; Length 757;
Best Local Similarity 100.0%; Pred. No. 1e-65; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAATAGGAAGATC 60
DB 141 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAATAGGAAGATC 200
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 201 TCAGTGCAGAGGCTCGCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 260
QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAGTGGGTT 180
DB 261 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAGTGGGTT 320
QY 181 CAGGATTCATGGACCACTTGACCAAGCAAAACCCAAATCCGAAGACT 228
DB 321 CAGGATTCATGGACCACTTGACCAAGCAAAACCCAAATCCGAAGACT 368

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Job time : 256 secs

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:49:12 ; Search time 1941 Seconds
(without alignments)
4133.145 Million cell updates/sec

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Perfect score: 228
Sequence: 1 cagccagatgcatcaatgc.....aaacccaactcgaagact 228

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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76: /cgn2_6/ptodata/2/pna/us6020 COMB.seq.*
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78: /cgn2_6/ptodata/2/pna/us6022 COMB.seq.*
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80: /cgn2_6/ptodata/2/pna/us6023B COMB.seq.*
81: /cgn2_6/ptodata/2/pna/us6024 COMB.seq.*
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110: /cgn2_6/ptodata/2/pna/us6053 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 228 | 100.0 | 228 | 48 | US-10-276-971-3 |
| 2 | 228 | 100.0 | 294 | 51 | US-10-449-831A-209 |
| 3 | 228 | 100.0 | 348 | 20 | US-09-442-384A-161 |
| 4 | 228 | 100.0 | 348 | 20 | US-09-442-384B-161 |
| 5 | 228 | 100.0 | 349 | 16 | US-09-221-481-519 |
| 6 | 228 | 100.0 | 349 | 20 | US-09-442-366A-1139 |
| 7 | 228 | 100.0 | 349 | 20 | US-09-442-384A-161 |
| 8 | 228 | 100.0 | 349 | 20 | US-09-442-589A-37 |
| 9 | 228 | 100.0 | 349 | 20 | US-09-442-589B-37 |
| 10 | 228 | 100.0 | 392 | 22 | US-09-534-843-7971 |
| 11 | 228 | 100.0 | 403 | 17 | US-09-287-618-15642 |
| 12 | 228 | 100.0 | 405 | 51 | US-10-449-831A-213 |
| 13 | 228 | 100.0 | 425 | 17 | US-09-287-618-16749 |
| 14 | 228 | 100.0 | 437 | 31 | US-09-726-791-973 |
| 15 | 228 | 100.0 | 454 | 22 | US-09-534-843-7953 |
| 16 | 228 | 100.0 | 457 | 17 | US-09-287-618-25718 |
| 17 | 228 | 100.0 | 459 | 33 | US-09-823-301-8626 |
| 18 | 228 | 100.0 | 468 | 22 | US-09-534-843-7980 |
| 19 | 228 | 100.0 | 475 | 1 | PCT-US02-02781-3105 |
| 20 | 228 | 100.0 | 475 | 44 | US-10-060-036-3105 |
| 21 | 228 | 100.0 | 482 | 31 | US-09-726-791-1183 |
| 22 | 228 | 100.0 | 482 | 33 | US-09-823-301-7586 |
| 23 | 228 | 100.0 | 491 | 27 | US-09-652-109-4628 |
| 24 | 228 | 100.0 | 492 | 22 | US-09-534-843-7975 |
| 25 | 228 | 100.0 | 496 | 22 | US-09-534-843-7976 |
| 26 | 228 | 100.0 | 512 | 31 | US-09-726-791-1190 |
| 27 | 228 | 100.0 | 513 | 31 | US-09-721-588-3578 |
| 28 | 228 | 100.0 | 516 | 31 | US-09-721-588-1376 |
| 29 | 228 | 100.0 | 520 | 22 | US-09-534-843-7960 |
| 30 | 228 | 100.0 | 521 | 29 | US-09-699-998-7783 |
| 31 | 228 | 100.0 | 522 | 22 | US-09-534-843-7963 |
| 32 | 228 | 100.0 | 530 | 33 | US-09-823-301-6829 |
| 33 | 228 | 100.0 | 532 | 22 | US-09-534-843-7951 |
| 34 | 228 | 100.0 | 545 | 22 | US-09-534-843-7954 |
| 35 | 228 | 100.0 | 557 | 30 | US-09-710-286-1702 |
| 36 | 228 | 100.0 | 559 | 27 | US-09-652-128-6130 |
| 37 | 228 | 100.0 | 565 | 33 | US-09-824-130-501 |
| 38 | 228 | 100.0 | 572 | 22 | US-09-534-843-7962 |
| 39 | 228 | 100.0 | 582 | 22 | US-09-534-843-7965 |
| 40 | 228 | 100.0 | 584 | 22 | US-09-534-843-7958 |
| 41 | 228 | 100.0 | 588 | 31 | US-09-721-588-2472 |
| 42 | 228 | 100.0 | 591 | 22 | US-09-534-843-7967 |
| 43 | 228 | 100.0 | 647 | 32 | US-09-777-430A-72 |
| 44 | 228 | 100.0 | 680 | 27 | US-09-652-128-8614 |
| 45 | 228 | 100.0 | 682 | 29 | US-09-699-998-7825 |

ALIGNMENTS

RESULT 1
 US-10-276-971-3
 ; Sequence 3, Application US/10276971
 ; GENERAL INFORMATION:
 ; APPLICANT: Egashira Kensuke
 ; APPLICANT: Yoshikazu Yonemitsu
 ; APPLICANT: Katsuo Sueishi
 ; APPLICANT: Yasuhiro Ikeda
 ; APPLICANT: Yoshiyuki Inada
 ; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
 ; FILE REFERENCE: 2733 USOP
 ; CURRENT APPLICATION NUMBER: US/10/276,971
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 4
 ; SEQ ID NO 3
 ; LENGTH: 228
 ; TYPE: DNA
 ; ORGANISM: Human

Query Match 100.0%; Score 228; DB 48; Length 228;
 Best Local Similarity 100.0%; Pred. No. 6,9e-58;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
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| Qy | 1 | CAGCCAGATCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAGATC | 60 |
| Db | 1 | CAGCCAGATCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAGATC | 60 |
| Qy | 61 | TCAGTCGAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT | 120 |
| Db | 61 | TCAGTCGAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT | 120 |
| Qy | 121 | GTGATCTTCAAGACCAATTTGGCCAAAGGAGATCTGTGACCCCAAGCAGAGTGGGTT | 180 |
| Db | 121 | GTGATCTTCAAGACCAATTTGGCCAAAGGAGATCTGTGACCCCAAGCAGAGTGGGTT | 180 |
| Qy | 181 | CAGGATTCATGACCACTGGCAAGCAACCAAACTCCGAAGACT | 228 |
| Db | 181 | CAGGATTCATGACCACTGGCAAGCAACCAAACTCCGAAGACT | 228 |

RESULT 2
 US-10-449-831A-209
 ; Sequence 209, Application US/10449831A
 ; GENERAL INFORMATION:
 ; APPLICANT: Koentgen, Frank
 ; TITLE OF INVENTION: Higher molecular weight entities and uses therefor
 ; FILE REFERENCE: 2385978
 ; CURRENT APPLICATION NUMBER: US/10/449,831A
 ; CURRENT FILING DATE: 2003-05-30
 ; PRIOR APPLICATION NUMBER: USSN 60/384878
 ; PRIOR FILING DATE: 2002-05-31
 ; NUMBER OF SEQ ID NOS: 237
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 209
 ; LENGTH: 294
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(294)
 US-10-449-831A-209

Query Match 100.0%; Score 228; DB 51; Length 294;
 Best Local Similarity 100.0%; Pred. No. 7,5e-58;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | CAGCCAGATCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAGATC | 60 |
| Db | 67 | CAGCCAGATCAATCAATGCCCGAGTCACCTGCTGTATATACTTACCAATAGGAGATC | 126 |
| Qy | 61 | TCAGTCGAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT | 120 |
| Db | 127 | TCAGTCGAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT | 186 |
| Qy | 121 | GTGATCTTCAAGACCAATTTGGCCAAAGGAGATCTGTGACCCCAAGCAGAGTGGGTT | 180 |
| Db | 187 | GTGATCTTCAAGACCAATTTGGCCAAAGGAGATCTGTGACCCCAAGCAGAGTGGGTT | 246 |
| Qy | 181 | CAGGATTCATGACCACTGGCAAGCAACCAAACTCCGAAGACT | 228 |
| Db | 247 | CAGGATTCATGACCACTGGCAAGCAACCAAACTCCGAAGACT | 294 |

RESULT 3
 US-09-442-384A-161
 ; Sequence 161, Application US/09442384A
 ; GENERAL INFORMATION:
 ; APPLICANT: Chencnik, Alex
 ; APPLICANT: Lukashiev, Matvey
 ; TITLE OF INVENTION: Hematology/Immunology Array

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; CURRENT APPLICATION NUMBER: US/09/442,384A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384A-161

Query Match      100.0%; Score 228; DB 20; Length 348;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATTAATTCACCAATAGGAAGATC 60
Db 104 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATTAATTCACCAATAGGAAGATC 163

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db 164 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 223

QY 121 GTGATCTTCAAGACCAATGTGGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 180
Db 224 GTGATCTTCAAGACCAATGTGGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 283

QY 181 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCGAAGACT 331

RESULT 4
US-09-442-384B-161
; Sequence 161, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: US/09/442,384B
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384B-161

Query Match      100.0%; Score 228; DB 20; Length 348;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATTAATTCACCAATAGGAAGATC 60
Db 104 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATTAATTCACCAATAGGAAGATC 163

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db 164 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 223

QY 121 GTGATCTTCAAGACCAATGTGGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 180
Db 224 GTGATCTTCAAGACCAATGTGGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 283

QY 181 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCGAAGACT 331

RESULT 5
US-09-221-481-519
; Sequence 519, Application US/09221481
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-008CIP6
; CURRENT FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 519
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-221-481-519

Query Match      100.0%; Score 228; DB 16; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATTAATTCACCAATAGGAAGATC 60
Db 104 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATTAATTCACCAATAGGAAGATC 163

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db 164 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 223

QY 121 GTGATCTTCAAGACCAATGTGGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 180
Db 224 GTGATCTTCAAGACCAATGTGGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 283

QY 181 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCGAAGACT 331

RESULT 6
US-09-442-366A-1139
; Sequence 1139, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-008CIP13
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: US/09/442,366A
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1139
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-1139

Query Match      100.0%; Score 228; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATTAATTCACCAATAGGAAGATC 60
Db 104 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATTAATTCACCAATAGGAAGATC 163

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db 164 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 223

QY 121 GTGATCTTCAAGACCAATGTGGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 180
Db 224 GTGATCTTCAAGACCAATGTGGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 283
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Db 104 CAGCCAGATGCAATCAATGCCAGTCACTGCTGTTTAACTTCAACATAGGAAGATC 163
Qy 61 TCAGTGAGAGGCTCGGAGCTATAGAAAGATCAGCAGCAGCAAGTGTCCCAAGAGGCT 120
Db 164 TCAGTGAGAGGCTCGGAGCTATAGAAAGATCAGCAGCAGCAAGTGTCCCAAGAGGCT 223
Qy 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 224 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 283
Qy 181 CAGGATTCATGGACCACTGGCAAGCAAAACCAAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGGCAAGCAAAACCAAACTCCGAAGACT 331

RESULT 7

US-09-442-384-161
; Sequence 161, Application US/09442384
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384-161

Query Match 100.0%; Score 228; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGATGCAATCAATGCCAGTCACTGCTGTTTAACTTCAACATAGGAAGATC 60
Db 104 CAGCCAGATGCAATCAATGCCAGTCACTGCTGTTTAACTTCAACATAGGAAGATC 163
Qy 61 TCAGTGAGAGGCTCGGAGCTATAGAAAGATCAGCAGCAGCAAGTGTCCCAAGAGGCT 120
Db 164 TCAGTGAGAGGCTCGGAGCTATAGAAAGATCAGCAGCAGCAAGTGTCCCAAGAGGCT 223
Qy 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 224 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 283
Qy 181 CAGGATTCATGGACCACTGGCAAGCAAAACCAAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGGCAAGCAAAACCAAACTCCGAAGACT 331

RESULT 8

US-09-442-589A-37
; Sequence 37, Application US/09442589A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Human Cardiovascular Array
; FILE REFERENCE: CLON-006CIP10
; CURRENT APPLICATION NUMBER: US/09/442,589A
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 597
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 37
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleic acid probe
US-09-442-589A-37

Query Match 100.0%; Score 228; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGATGCAATCAATGCCAGTCACTGCTGTTTAACTTCAACATAGGAAGATC 60
Db 104 CAGCCAGATGCAATCAATGCCAGTCACTGCTGTTTAACTTCAACATAGGAAGATC 163
Qy 61 TCAGTGAGAGGCTCGGAGCTATAGAAAGATCAGCAGCAGCAAGTGTCCCAAGAGGCT 120
Db 164 TCAGTGAGAGGCTCGGAGCTATAGAAAGATCAGCAGCAGCAAGTGTCCCAAGAGGCT 223
Qy 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 224 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 283
Qy 181 CAGGATTCATGGACCACTGGCAAGCAAAACCAAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGGCAAGCAAAACCAAACTCCGAAGACT 331

RESULT 9

US-09-442-589B-37
; Sequence 37, Application US/09442589B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Human Cardiovascular Array
; FILE REFERENCE: CLON-006CIP10
; CURRENT APPLICATION NUMBER: US/09/442,589B
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1194
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleic acid probe
US-09-442-589B-37

Query Match 100.0%; Score 228; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGATGCAATCAATGCCAGTCACTGCTGTTTAACTTCAACATAGGAAGATC 60
Db 104 CAGCCAGATGCAATCAATGCCAGTCACTGCTGTTTAACTTCAACATAGGAAGATC 163
Qy 61 TCAGTGAGAGGCTCGGAGCTATAGAAAGATCAGCAGCAGCAAGTGTCCCAAGAGGCT 120
Db 164 TCAGTGAGAGGCTCGGAGCTATAGAAAGATCAGCAGCAGCAAGTGTCCCAAGAGGCT 223
Qy 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 224 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 283
Qy 181 CAGGATTCATGGACCACTGGCAAGCAAAACCAAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGGCAAGCAAAACCAAACTCCGAAGACT 331

RESULT 10

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US-09-534-843-7971
; Sequence 7971, Application US/09534843
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLECULE
; FILE REFERENCE: PD-1007 CIP
; CURRENT APPLICATION NUMBER: US/09/534,843
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 49783
; SOFTWARE: PERL Program
; SEQ ID NO 7971
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu01345546
US-09-534-843-7971

Query Match      100.0%; Score 228; DB 22; Length 392;
Best Local Similarity 100.0%; Pred. No. 8.2e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 60
DB      126 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 185

QY      61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB      186 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 245

QY      121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTCTGCTGATTAACCTTCCCAAGAAGCT 180
DB      246 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTCTGCTGATTAACCTTCCCAAGAAGCT 305

QY      181 CAGGATTCATGGACCATCTGGACAAAGCAAGCAACCAAACTCCGAAGACT 228
DB      306 CAGGATTCATGGACCATCTGGACAAAGCAAGCAACCAAACTCCGAAGACT 353

RESULT 11
US-09-287-618-15642
; Sequence 15642, Application US/09287618
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-768
; CURRENT APPLICATION NUMBER: US/09/287,618
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 15642
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(403)
; OTHER INFORMATION: n = A,T,C or G
US-09-287-618-15642

Query Match      100.0%; Score 228; DB 17; Length 403;
Best Local Similarity 100.0%; Pred. No. 8.3e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 60
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DB      118 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 177
QY      61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB      178 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 237
QY      121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTCTGCTGATTAACCTTCCCAAGAAGCT 180
DB      238 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTCTGCTGATTAACCTTCCCAAGAAGCT 297
QY      181 CAGGATTCATGGACCATCTGGACAAAGCAAGCAACCAAACTCCGAAGACT 228
DB      298 CAGGATTCATGGACCATCTGGACAAAGCAAGCAACCAAACTCCGAAGACT 345

RESULT 12
US-10-449-831A-213
; Sequence 213, Application US/10449831A
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; TITLE OF INVENTION: Higher molecular weight entities and uses therefor
; FILE REFERENCE: 2385978
; CURRENT APPLICATION NUMBER: US/10/449,831A
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: USSN 60/384878
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 213
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human MCP-1 chimeric construct
; NAME/KEY: CDS
; LOCATION: (1)_(399)
US-10-449-831A-213
```

```
Query Match      100.0%; Score 228; DB 51; Length 405;
Best Local Similarity 100.0%; Pred. No. 8.3e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 60
DB      145 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 204
QY      61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB      205 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 264
QY      121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTCTGCTGATTAACCTTCCCAAGAAGCT 180
DB      265 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTCTGCTGATTAACCTTCCCAAGAAGCT 324
QY      181 CAGGATTCATGGACCATCTGGACAAAGCAAGCAACCAAACTCCGAAGACT 228
DB      325 CAGGATTCATGGACCATCTGGACAAAGCAAGCAACCAAACTCCGAAGACT 372
```

```
RESULT 13
US-09-287-618-16749
; Sequence 16749, Application US/09287618
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-768
; CURRENT APPLICATION NUMBER: US/09/287,618
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: Fast-SEQ for Windows Version 3.0
```

; SEQ ID NO 16749

; LENGTH: 425

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-287-618-16749

Query Match 100.0%; Score 228; DB 17; Length 425;
Best Local Similarity 100.0%; Pred. No. 8.4e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAGATC 60
DB 123 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAGATC 182
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 242
QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 243 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 302
QY 181 CAGGATTCATGGACCACTGTGACAAAGCAAGCAAACTCCGAAGACT 228
DB 303 CAGGATTCATGGACCACTGTGACAAAGCAAGCAAACTCCGAAGACT 350

RESULT 14

US-09-726-791-973

; Sequence 973, Application US/09726791

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Holtzman, Douglas A.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

; FILE REFERENCE: 1600.2009-001

; CURRENT APPLICATION NUMBER: US/09/726,791

; CURRENT FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: 60/168,127

; PRIOR FILING DATE: 1999-11-30

; NUMBER OF SEQ ID NOS: 1870

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 973

; LENGTH: 437

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(437)

; OTHER INFORMATION: n = A,T,C or G

US-09-726-791-973

Query Match 100.0%; Score 228; DB 31; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.5e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAGATC 60
DB 132 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAGATC 191
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 192 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 251
QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 252 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 311
QY 181 CAGGATTCATGGACCACTGTGACAAAGCAAGCAAACTCCGAAGACT 228
DB 312 CAGGATTCATGGACCACTGTGACAAAGCAAGCAAACTCCGAAGACT 359

RESULT 15

US-09-534-843-7953

; Sequence 7953, Application US/09534843

; GENERAL INFORMATION:

; APPLICANT: Seilhamer, Jeffrey J.

; APPLICANT: Deleage, Angelo M.

; APPLICANT: Stuart, Susan G.

; APPLICANT: Stuve, Laura L.

; APPLICANT: Mullaly, Sara J.

; APPLICANT: Naughton, Rebecca E.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLEC

; FILE REFERENCE: PD-1007 CIP

; CURRENT APPLICATION NUMBER: US/09/534,843

; CURRENT FILING DATE: 2000-03-24

; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 49783

; SOFTWARE: PERL Program

; SEQ ID NO 7953

; LENGTH: 454

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: hu01000080

US-09-534-843-7953

Query Match 100.0%; Score 228; DB 22; Length 454;

Best Local Similarity 100.0%; Pred. No. 8.6e-58;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAGATC 60
DB 123 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAGATC 182
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT 242
QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 243 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 302
QY 181 CAGGATTCATGGACCACTGTGACAAAGCAAGCAAACTCCGAAGACT 228
DB 303 CAGGATTCATGGACCACTGTGACAAAGCAAGCAAACTCCGAAGACT 350

Search completed: August 31, 2004, 04:19:46

Job time : 1944 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:49:12 ; Search time 1465 Seconds

(without alignments)
4647.493 Million cell updates/sec

Title: 07330446

Perfect score: 228

Sequence: 1 cagccagatgcaatcaatgc.....aaacccaactccgaagact 228

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pig:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 228 | 100.0 | 432 | 9 | AV661469 |
| 2 | 228 | 100.0 | 497 | 9 | AA047099 |
| 3 | 228 | 100.0 | 513 | 9 | AV714555 |
| 4 | 228 | 100.0 | 549 | 13 | BA490080 |

| | | | | | |
|------|-----|-------|-----|----|----------|
| 5 | 228 | 100.0 | 563 | 12 | BM704915 |
| 6 | 228 | 100.0 | 588 | 12 | BM708613 |
| 7 | 228 | 100.0 | 593 | 12 | BM888255 |
| 8 | 228 | 100.0 | 594 | 13 | BQ631442 |
| | 228 | 100.0 | 616 | 9 | AL697816 |
| C 10 | 228 | 100.0 | 623 | 10 | AW772091 |
| C 11 | 228 | 100.0 | 628 | 13 | BU730951 |
| C 12 | 228 | 100.0 | 634 | 13 | BQ631169 |
| C 13 | 228 | 100.0 | 640 | 12 | BM973445 |
| C 14 | 228 | 100.0 | 640 | 13 | BU685364 |
| C 15 | 228 | 100.0 | 644 | 13 | BQ573817 |
| C 16 | 228 | 100.0 | 647 | 14 | CD638814 |
| 17 | 228 | 100.0 | 649 | 14 | CB267966 |
| 18 | 228 | 100.0 | 652 | 10 | BF339323 |
| 19 | 228 | 100.0 | 657 | 9 | AV661137 |
| 20 | 228 | 100.0 | 670 | 14 | CD686424 |
| 21 | 228 | 100.0 | 673 | 14 | CD638839 |
| 22 | 228 | 100.0 | 673 | 14 | CD640282 |
| 23 | 228 | 100.0 | 683 | 10 | BF343817 |
| 24 | 228 | 100.0 | 691 | 14 | CD641143 |
| 25 | 228 | 100.0 | 708 | 14 | CD523445 |
| 26 | 228 | 100.0 | 710 | 14 | CD641497 |
| C 27 | 228 | 100.0 | 713 | 14 | CA440694 |
| 28 | 228 | 100.0 | 713 | 14 | CD641186 |
| 29 | 228 | 100.0 | 720 | 14 | CD640058 |
| 30 | 228 | 100.0 | 723 | 14 | CD522423 |
| 31 | 228 | 100.0 | 727 | 9 | AV716926 |
| C 32 | 228 | 100.0 | 732 | 12 | BQ001668 |
| C 33 | 228 | 100.0 | 737 | 14 | CA307389 |
| 34 | 228 | 100.0 | 738 | 14 | CD641135 |
| 35 | 228 | 100.0 | 745 | 9 | AV717442 |
| 36 | 228 | 100.0 | 745 | 13 | BU199251 |
| C 37 | 228 | 100.0 | 751 | 14 | CA448393 |
| 38 | 228 | 100.0 | 754 | 14 | CD520218 |
| 39 | 228 | 100.0 | 762 | 9 | AV733621 |
| 40 | 228 | 100.0 | 766 | 13 | BQ224954 |
| C 41 | 228 | 100.0 | 787 | 13 | BU192217 |
| 42 | 228 | 100.0 | 789 | 14 | CD522574 |
| 43 | 228 | 100.0 | 794 | 13 | BQ432639 |
| 44 | 228 | 100.0 | 824 | 13 | BU601003 |
| 45 | 228 | 100.0 | 852 | 10 | BF211527 |

ALIGNMENTS

RESULT 1

AV661469

LOCUS

AV661469

DEFINITION

AV661469

ACCESSION

AV661469.1

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

AV661469 432 bp mRNA linear EST 16-JAN-2002
AV661469 GLC Homo sapiens cDNA clone GLCGSG05 3', mRNA sequence.

AV661469.1 GI:9882483

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 432)

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,

Xiao,H., Gu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,

Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,

Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level

by comparing gene expression profiles of hepatocellular carcinoma

with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

21625106

11752456

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919 (ex.45)

Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source

FEATURES

source

High quality sequence stop: 487.

Location/Qualifiers

1..497

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3803121"

/db_xref="taxon:9606"

/clone="IMAGE:488534"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares pregnant uterus NbHPU"

/note="Organ: uterus; Vector: pT73-Pac; Site: 1: Not I;

Site 2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5',

ACTGGAAGATTCGGCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 228; DB 9; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.2e-52;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCATAGGAGATC 60

Db 116 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCATAGGAGATC 175

QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120

Db 176 TCAGTGCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 235

QY 121 GTGATCTTCAGACCAATGTCGCCAAGAGATCTGTGTCGACCCAGCAGCAAGTGTGGTT 180

Db 236 GTGATCTTCAGACCAATGTCGCCAAGAGATCTGTGTCGACCCAGCAGCAAGTGTGGTT 295

QY 181 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAGACT 228

Db 296 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAGACT 343

RESULT 2

AA047099

LOCUS

DEFINITION

2k74a08.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone

IMAGE:488534 5' similar to gb:M24545 MONOCYTE CHEMOTACTIC PROTEIN 1

PRECUSOR (HUMAN); mRNA sequence.

AA047099

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 497)

REFERENCE

AUTHORS

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

PUBMED

COMMENT

Contact: Wilton PK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through INL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 741 Std Error: 0.00

Seq primer: -28M3 rev2 from Amersham

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

source

FEATURES

source

High quality sequence stop: 487.

Location/Qualifiers

1..497

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3803121"

/db_xref="taxon:9606"

/clone="IMAGE:488534"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares pregnant uterus NbHPU"

/note="Organ: uterus; Vector: pT73-Pac; Site: 1: Not I;

Site 2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5',

ACTGGAAGATTCGGCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 228; DB 9; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.2e-52;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCATAGGAGATC 60

Db 116 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAACCTCACCATAGGAGATC 175

QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120

Db 176 TCAGTGCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 235

QY 121 GTGATCTTCAGACCAATGTCGCCAAGAGATCTGTGTCGACCCAGCAGCAAGTGTGGTT 180

Db 236 GTGATCTTCAGACCAATGTCGCCAAGAGATCTGTGTCGACCCAGCAGCAAGTGTGGTT 295

QY 181 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAGACT 228

Db 296 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAGACT 343

RESULT 2

AA047099

LOCUS

DEFINITION

2k74a08.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone

IMAGE:488534 5' similar to gb:M24545 MONOCYTE CHEMOTACTIC PROTEIN 1

PRECUSOR (HUMAN); mRNA sequence.

AA047099

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 497)

REFERENCE

AUTHORS

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

PUBMED

COMMENT

Contact: Wilton PK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through INL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 741 Std Error: 0.00

Seq primer: -28M3 rev2 from Amersham

Query Match 100.0%; Score 228; DB 13; Length 549;
 Best Local Similarity 100.0%; Pred. No. 1.2e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 60
 DB 138 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 197

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
 DB 198 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 257

QY 121 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
 DB 258 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 317

QY 181 CAGGATTCATGAGCACCCTGGACAGCAAAACCCAACTCCGAGAGCT 228
 DB 318 CAGGATTCATGAGCACCCTGGACAGCAAAACCCAACTCCGAGAGCT 365

RESULT 5
 BM704915 563 bp mRNA linear EST 28-FEB-2002
 LOCUS UI-E-CII-afg-h-04-0-UI.r1 UI-E-CII Homo sapiens cDNA clone
 DEFINITION UI-E-CII-afg-h-04-0-UI 5', mRNA sequence.

ACCESSION BM704915
 VERSION BM704915.1 GI:19018173
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 563)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bentto-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..563
 /Organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-CII-afg-h-04-0-UI"
 /tissue_type="RPE and Choroid"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-CII"
 /note="Organ: eye; Vector: pRT3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-E-CII is a normalized cDNA library containing the
 following tissue(s): RPE and Choroid. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I

/mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DCBADG05"
 /cell_type="dendritic cells"
 /dev_stage="mature"
 /lab_host="BM25.8"
 /clone_lib="DCB"
 /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Query Match 100.0%; Score 228; DB 9; Length 513;
 Best Local Similarity 100.0%; Pred. No. 1.2e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 60
 DB 134 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 193

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
 DB 194 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 253

QY 121 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
 DB 254 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 313

QY 181 CAGGATTCATGAGCACCCTGGACAGCAAAACCCAACTCCGAGAGCT 228
 DB 314 CAGGATTCATGAGCACCCTGGACAGCAAAACCCAACTCCGAGAGCT 361

RESULT 4
 BX490080 549 bp mRNA linear EST 04-SEP-2003
 LOCUS DKFZp686B1371_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 DEFINITION DKFZp686B1371 5', mRNA sequence.

ACCESSION BX490080
 VERSION BX490080.1 GI:31999304
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 549)
 AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbauer,S., Mewes,H.W.,
 Weil,B., Amid,C., Osanger,A., Pobo,G., Han,M. and Wiemann,S.
 TITLE EST (Ottenwaelder,B., Obermaier,B., Deutschenbauer,S., Mewes,H.W.,
 et al.)
 JOURNAL Unpublished (2003)
 COMMENT Contact: MIPS
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by MedGenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German Genome Project. No sl sequence
 available.
 This clone (DKFZp686B1371) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 1..549
 /Organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp686B1371"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="686 (synonym: hlcc3)"
 /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN

adaptor, digested with Not I, and cloned directionally into pTV2132 vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (sequence that is located between the Not I site and the GATC tail). The sequence tag for this library is ACCGAC. This library was created for the program, Gene discovery in the Visual System, supported by National Eye Institute (NIH).

ORIGIN

| Query Match | 100.0% | Score 228 | DB 12 | Length 563 |
|-----------------------|----------------|--|----------|------------|
| Best Local Similarity | 100.0% | Pred. No. 1.3e-52 | | |
| Matches 228 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1 | CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTTATAACTTCACCAATAGGAAGATC | 60 | |
| Db | 108 | CAGCCAGATGCATCAATGCCCCCAGTCACCTGCTGTTTATAACTTCACCAATAGGAAGATC | 167 | |
| QY | 61 | TCAGTGCAGAGGCTGCGAGGTATAGAGAATCACCGACGCAAGTGTCCCAAGAAGCT | 120 | |
| Db | 168 | TCAGTGCAGAGGCTGCGAGGTATAGAGAATCACCGACGCAAGTGTCCCAAGAAGCT | 227 | |
| QY | 121 | GTGATCTTCAAGACCATTTGCGCAAGAGATCTGTGCTGACCCCAAGCAGAGATGGGTT | 180 | |
| Db | 228 | GTGATCTTCAAGACCATTTGCGCAAGAGATCTGTGCTGACCCCAAGCAGAGATGGGTT | 287 | |
| QY | 181 | CAGGATTCATGGACCACTGGACAGCAACCAACCTCCGAAGACT | 228 | |
| Db | 288 | CAGGATTCATGGACCACTGGACAGCAACCAACCTCCGAAGACT | 335 | |

| | | | | | |
|------------|---------------------------|--|--------|------|-----------------|
| RESULT 6 | BM708613 | linear | 588 bp | mrna | EST 28-FEB-2002 |
| LOCUS | BM708613 | | | | |
| DEFINITION | UI-B-CII-atw-i-08-0-UI-r1 | UI-E-CII Homo sapiens cDNA clone | | | |
| ACCESSION | BM708613 | UI-B-CII-atw-i-08-0-UI 5', mRNA sequence. | | | |
| VERSION | BM708613.1 | GI:19021871 | | | |
| KEYWORDS | | EST. | | | |
| SOURCE | | Homo sapiens (human) | | | |
| ORGANISM | | Homo sapiens | | | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| AUTHORS | | 1 (bases 1 to 588) | | | |
| TITLE | | Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery | | | |
| JOURNAL | | Genome Res. 6 (9), 791-806 (1996) | | | |
| MEDLINE | | 97044477 | | | |
| PUBMED | | 889548 | | | |
| COMMENT | | Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Dr. Gregg Hageman CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com). Seq primer: M13 Reverse. | | | |

| FEATURES | SOURCE |
|--------------------|--------|
| 1. <i>General</i> | |
| 2. <i>Specific</i> | |
| 3. <i>Other</i> | |
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| 98. <i>Other</i> | |
| 99. <i>Other</i> | |
| 100. <i>Other</i> | |

ORIGIN

| | Query Match | 100.0%; | Score 228; | DB 12; | Length 588; |
|----|-----------------------|---|--------------------|-----------|-------------|
| | Best Local Similarity | 100.0%; | Pred. No. 1.3e-52; | | |
| | Matches 228; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | CAGCCAGATGCAATCAATGCCGCCAGTCACCTGCTGTTATTAACCTCCACCAATAGGAAGATC | 60 | | |
| Db | 108 | CAGCCAGATGCAATCAATGCCGCCAGTCACCTGCTGTTATTAACCTCCACCAATAGGAAGATC | 167 | | |
| QY | 61 | TCAGTGCAGAGGCTCGCGACTATACAGAAATCAACAGCAGCAAGTGTGCCAAAGAAAGCT | 120 | | |
| Db | 168 | TCAGTGCAGAGGCTCGCGAGCTATAGAGAAATCAGCAGCAGCAAGTGTGCCAAAGAAAGCT | 227 | | |
| QY | 121 | GTGATCTTCAAGACCATTTGGCGCAGGAGATCTGTGCTGACCCCAAGCAGCAAGTGGGTT | 180 | | |
| Db | 228 | GTGATCTTCAAGACCATTTGGCGCAGGAGATCTGTGCTGACCCCAAGCAGCAAGTGGGTT | 287 | | |
| QY | 181 | CAGGATTCATGGACCACTGGACAGCAAAACCCAAACTCCGAAGACT | 228 | | |
| Db | 288 | CAGGATTCATGGACCACTGGACAGCAAAACCCAAACTCCGAAGACT | 335 | | |

| | | | |
|------------|-----------|-----------|---------|
| RESULT 7 | ACCESSION | REFERENCE | JOURNAL |
| BM888255 | VERSION | AUTHORS | COMMENT |
| LOCUS | KEYWORDS | TITLE | |
| DEFINITION | SOURCE | | |
| | ORGANISM | | |

FEATURES

```

/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/tissue_type="eye"
/cell_type="trabecular meshwork"

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/lab host="TOP10P."
/clone lib="Human Trabecular Meshwork cDNA library"
/note=vector: pcDNA3; Site 1: EcoRI; Site 2: EcoRI; Human
cDNA library made from mRNA isolated from trabecular
meshwork cells established from eyes from 6 individuals,
ages 2 weeks to 2 years. Cells were harvested at passages
3 through 6. Invitrogen made a unidirectional cDNA library
from the mRNA from the frozen cells using a pcDNA3 vector
and TP010P, host cells."

ORIGIN
Query Match 100.0%; Score 228; DB 12; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTTTAACTTCAACCAATAGGAAGATC 60
DB 124 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTTTAACTTCAACCAATAGGAAGATC 183
QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGATGTCCCAAGAGCT 120
DB 184 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGATGTCCCAAGAGCT 243
QY 121 GTGATCTTCAAGACCATTTGTGCCAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 244 GTGATCTTCAAGACCATTTGTGCCAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 303
QY 181 CAGGATTCATGACCACTGCGACCAAGCAACCCAAATCCGAAGACT 228
DB 304 CAGGATTCATGACCACTGCGACCAAGCAACCCAAATCCGAAGACT 351

RESULT 8
BQ631442 594 bp mRNA linear EST 02-JUL-2002
LOCUS il17e04.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6030414 5'
DEFINITION similar to SW:SY02 HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2
PRECUSOR ;, mRNA sequence.

ACCESSION BQ631442.1 GI:21682960
VERSION BQ631442.1
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 594)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: il17e04.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@wustl.edu)

Seq primer: -40RP from Gibco
High quality sequence stop: 485.

Location/Qualifiers
1. .594
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

/db_xref="taxon:9606"
/clone="IMAGE:6030414"
/issue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 228; DB 13; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTTTAACTTCAACCAATAGGAAGATC 60
DB 120 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTTTAACTTCAACCAATAGGAAGATC 179
QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 180 TCAGTGCAGAGGCTCGGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAGCT 239
QY 121 GTGATCTTCAAGACCATTTGTGCCAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 240 GTGATCTTCAAGACCATTTGTGCCAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 239
QY 181 CAGGATTCATGACCACTGCGACCAAGCAACCCAAATCCGAAGACT 228
DB 300 CAGGATTCATGACCACTGCGACCAAGCAACCCAAATCCGAAGACT 347

RESULT 9

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

MIPI

INGOLSTAEDTER

THIS IS THE

CLONE FROM

RESEARCH CENTER

SEQUENCED BY

AVAILABLE.

PLEASE CONTACT

BERLIN-CHARLOTTENBURG

FEATURES

source

ORIGIN

Query Match 100.0%; Score 228; DB 9; Length 616;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCACCAATAGGAGATC 60
Db 134 CAGCCAGATCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCACCAATAGGAGATC 193

QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db 194 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 253

QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 180
Db 254 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 313

QY 181 CAGGATTCATGACCACTGGACAGCAAAACCCAAACTCCGAAGACT 228
Db 314 CAGGATTCATGACCACTGGACAGCAAAACCCAAACTCCGAAGACT 361

RESULT 10
AW772091/c
LOCUS
DEFINITION
h67c08.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3032942 3'
similar to gb:M24545 MONOCYTE CHEMOTACTIC PROTEIN 1 PRECURSOR
(HUMAN); mRNA sequence.

ACCESSION
AW772091
VERSION
AW772091.1 GI:7704153
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 623)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
Location/Qualifiers
1. 623
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3032942"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs

FEATURES
source

ORIGIN

Query Match 100.0%; Score 228; DB 10; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCACCAATAGGAGATC 60
Db 603 CAGCCAGATCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCACCAATAGGAGATC 544

QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db 543 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 484

QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 180
Db 483 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 424

QY 181 CAGGATTCATGACCACTGGACAGCAAAACCCAAACTCCGAAGACT 228
Db 423 CAGGATTCATGACCACTGGACAGCAAAACCCAAACTCCGAAGACT 376

RESULT 11
BU730951/c
LOCUS
DEFINITION
UI-E-C11-afw-i-08-0-UI.s1 UI-E-C11 Homo sapiens cDNA clone
UI-E-C11-afw-i-08-0-UI 3', mRNA sequence.

ACCESSION
BU730951
VERSION
BU730951.1 GI:23655357
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 628)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-33, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1. 628
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-C11-afw-i-08-0-UI"
/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phase resistant)"
/clone_lib="UIT-F-C11"

FEATURES
source

ORIGIN

Query Match 100.0%; Score 228; DB 10; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCACCAATAGGAGATC 60
Db 603 CAGCCAGATCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCACCAATAGGAGATC 544

QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db 543 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 484

QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 180
Db 483 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 424

QY 181 CAGGATTCATGACCACTGGACAGCAAAACCCAAACTCCGAAGACT 228
Db 423 CAGGATTCATGACCACTGGACAGCAAAACCCAAACTCCGAAGACT 376

RESULT 11
BU730951/c
LOCUS
DEFINITION
UI-E-C11-afw-i-08-0-UI.s1 UI-E-C11 Homo sapiens cDNA clone
UI-E-C11-afw-i-08-0-UI 3', mRNA sequence.

ACCESSION
BU730951
VERSION
BU730951.1 GI:23655357
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 628)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-33, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1. 628
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-C11-afw-i-08-0-UI"
/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phase resistant)"
/clone_lib="UIT-F-C11"

FEATURES
source

modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-CII is a normalized cDNA library containing the
following tissue(s): RPE and Choroid. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pRT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is ACCATA.
This library was created for the program, Gene Discovery
in the Visual System, supported by National Eye Institute
(NEI).
TAG TISSUE=RPE and Choroid
TAG LIB=UI-E-CII
TAG_SEQ=ACCTA"

ORIGIN
Query Match 100.0%; Score 228; DB 13; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACTCTCTTTATTAATTCACCAATAGGAGATC 60
DB 622 CAGCCAGATGCAATCAATGCCCGAGTCACTCTCTTTATTAATTCACCAATAGGAGATC 563
QY 61 TCAGTGCAGAGCTCGGAGCTATAGAGATCACAGCAGCAAGTGTCCCAAGAAAGCT 120
DB 562 TCAGTGCAGAGCTCGGAGCTATAGAGATCACAGCAGCAAGTGTCCCAAGAAAGCT 503
QY 121 GTGATCTTCAAGACCATTTGTGCCAAGGAGATCTGTGTCGCCCAAGCAAGTGGGTT 180
DB 502 GTGATCTTCAAGACCATTTGTGCCAAGGAGATCTGTGTCGCCCAAGCAAGTGGGTT 443
QY 181 CAGGATTCATGACACCTGCAGCAGCAACCAACTCCGAAGCT 228
DB 442 CAGGATTCATGACACCTGCAGCAGCAACCAACTCCGAAGCT 395

RESULT 12
BQ631169/c 634 bp mRNA linear EST 02-JUL-2002
LOCUS 1117e04.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6030414 3'
DEFINITION similar to SW:SY02 HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2
PRECUSOR ; mRNA sequence.
QY 1 CAGGATTCATGACACCTGCAGCAGCAACCAACTCCGAAGCT 228
DB 442 CAGGATTCATGACACCTGCAGCAGCAACCAACTCCGAAGCT 395
ACCESSION BQ631169.1 GI:21682687
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Secombe, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohph.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center for information on

obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 439.
FEATURES
source
1..634
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6030414"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-
selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning. Amplified
once. Contact information: Hiroshi Inoue, MD, Metabolism Div.
(Alan Permutt Lab), Washington University School of Medicine,
Box 8127, 660 South Euclid Ave., St. Louis, MO 63110,
E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916,
Fax: 314-747-2892."

ORIGIN

Query Match 100.0%; Score 228; DB 13; Length 634;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACTCTCTTTATTAATTCACCAATAGGAGATC 60
DB 607 CAGCCAGATGCAATCAATGCCCGAGTCACTCTCTTTATTAATTCACCAATAGGAGATC 548
QY 61 TCAGTGCAGAGCTCGGAGCTATAGAGATCACAGCAGCAAGTGTCCCAAGAAAGCT 120
DB 547 TCAGTGCAGAGCTCGGAGCTATAGAGATCACAGCAGCAAGTGTCCCAAGAAAGCT 488
QY 121 GTGATCTTCAAGACCATTTGTGCCAAGGAGATCTGTGTCGCCCAAGCAAGTGGGTT 180
DB 487 GTGATCTTCAAGACCATTTGTGCCAAGGAGATCTGTGTCGCCCAAGCAAGTGGGTT 428
QY 181 CAGGATTCATGACACCTGCAGCAGCAACCAACTCCGAAGCT 228
DB 427 CAGGATTCATGACACCTGCAGCAGCAACCAACTCCGAAGCT 380

RESULT 13
BQ973445/c 640 bp mRNA linear EST 20-FEB-2003
LOCUS UI-CF-EC1-abx-n-09-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
DEFINITION UI-CF-EC1-abx-n-09-0-UI 3', mRNA sequence.
QY 1 CAGGATTCATGACACCTGCAGCAGCAACCAACTCCGAAGCT 228
DB 427 CAGGATTCATGACACCTGCAGCAGCAACCAACTCCGAAGCT 380
ACCESSION BQ973445.1 GI:19591036
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 640)
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 1-36, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..640
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-EC1-abx-n-09-0-UI"
 /tissue_type="lung"
 /dev_stage="Adult and Fetal"
 /lab_host="DHI0B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EC1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-EC1 is a normalized cDNA library containing the
 following tissue(s): Normal lung from adult and from fetal
 day 64, day 87, week 19 and week 42. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 AAGTGCTTAC.
 TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
 and 380-383
 TAG_LIB=UI-CF-EC1
 TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 100.0%; Score 228; DB 12; Length 640;
 Best Local Similarity 100.0%; Pred. No. 1.3e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 60
 Db 619 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 560
 QY 61 TCAGTCCAGAGGCTCCGAGCTATAGAAATCACACAGCAGCAAGTGTCCCAAGAGCT 120
 Db 559 TCAGTCCAGAGGCTCCGAGCTATAGAAATCACACAGCAGCAAGTGTCCCAAGAGCT 500
 QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAAGTGGGTT 180
 Db 499 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAAGTGGGTT 440
 QY 181 CAGGATTCATGGACCACTGGACAGCAAGCAACCCAACTCCGAGACT 228
 Db 439 CAGGATTCATGGACCACTGGACAGCAAGCAACCCAACTCCGAGACT 392

RESULT 14

BU685364/c
 LOCUS
 DEFINITION UI-CF-DUI-aav-j-23-0-UI-s2 UI-CF-DUI Homo sapiens cDNA clone
 UI-CF-DUI-aav-j-23-0-UI 3', mRNA sequence.
 BU685364
 BU685364.1 GI:23539236
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 640)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 889548
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 1-35, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..640
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-DUI-aav-j-23-0-UI"
 /tissue_type="Primary Lung Epithelial Cells"
 /dev_stage="Adult"
 /lab_host="DHI0B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-DUI"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-DUI is a normalized cDNA library containing the
 following tissue(s): Primary Lung Epithelial Cells The
 library was constructed according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into pT7T3-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is GGCTGTAGGC.
 TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_LIB=UI-CF-DUI
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 100.0%; Score 228; DB 13; Length 640;
 Best Local Similarity 100.0%; Pred. No. 1.3e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 60
 Db 618 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 559
 QY 61 TCAGTCCAGAGGCTCCGAGCTATAGAAATCACACAGCAGCAAGTGTCCCAAGAGCT 120
 Db 558 TCAGTCCAGAGGCTCCGAGCTATAGAAATCACACAGCAGCAAGTGTCCCAAGAGCT 499
 QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAAGTGGGTT 180
 Db 498 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGAAGTGGGTT 439
 QY 181 CAGGATTCATGGACCACTGGACAGCAAGCAACCCAACTCCGAGACT 228
 Db 438 CAGGATTCATGGACCACTGGACAGCAAGCAACCCAACTCCGAGACT 391

RESULT 15

BQ573817/c
 LOCUS BQ573817.1
 DEFINITION UI-H-EZ0-bax-c-19-0-UI.s1 NCI CGAP Ch1 Homo sapiens CDNA clone
 ACCESSION BQ573817
 VERSION BQ573817
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 644)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs@mail.nih.gov
 Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
 Orthopaedics
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-39, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..644
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-EZ0-bax-c-19-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Ch1"
 /note="Organ: Left Pelvis; Vector: pTT73-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP Ch1 is a cDNA library containing the following
 tissue(s): Chondrosarcoma Grade II. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pTT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (GT)₁₈ tail. The sequence tag for this library is
 TGATCAGGCT.
 TAG_TISSUE=grade-2-chondrosarcoma
 TAG_LIB=UI-H-EZ0
 TAG_SEQ=ATCTAATATG

ORIGIN

Query Match 100.0%; Score 228; DB 13; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.3e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCAGTCACTGCTGTTTAACTTCACCAATAGGAATC 60
 DB 622 CAGCCAGATGCAATCAATGCCAGTCACTGCTGTTTAACTTCACCAATAGGAATC 563
 QY 61 TCAGTCAGAGGCTCGAGGCTATAGAGAAATCACCAGCAGCAAGTGTCCCAAAGGCT 120
 DB 562 TCAGTCAGAGGCTCGAGGCTATAGAGAAATCACCAGCAGCAAGTGTCCCAAAGGCT 503

QY 121 GTGATCTTCAAGACCATTTGTCGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
 DB 502 GTGATCTTCAAGACCATTTGTCGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 443
 QY 181 CAGGATTTCATGGACCACTTGGACACAAAGCAAGCAAACTCCGAAGACT 228
 DB 442 CAGGATTTCATGGACCACTTGGACACAAAGCAAGCAAACTCCGAAGACT 395

Search completed: August 31, 2004, 03:47:21
 Job time : 1473 secs

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